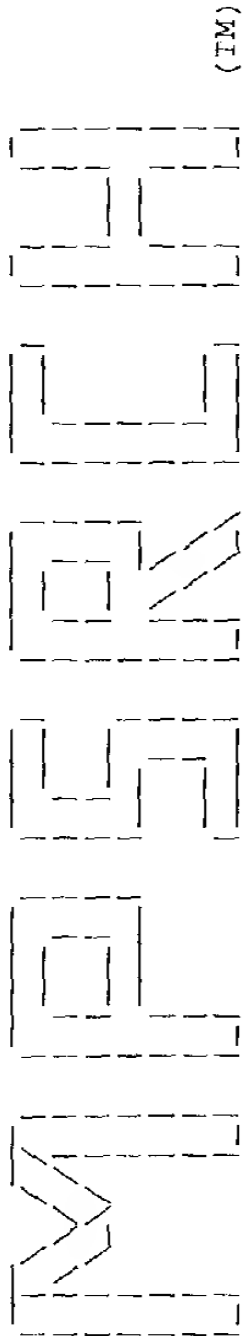


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(TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 17 11:16:36 2000; MasPar time 22.82 Seconds  
705.631 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-455-683-12  
Description: (1-295) from US08455683.pep  
Perfect Score: 2229  
Sequence: 1 YTKMKTATNIYIFNLALADA.....NTVQDPAYLREIDGMNKPV 295

Scoring table: PAM 150  
Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: sprembl9  
1:sp\_archaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle  
9:sp\_phase 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified  
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 47.211; Variance 119.565; scale 0.395

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1523	68.3	373	13	O57585	OPIOID RECEPTOR HOMO	5.90e-223
2	1461	65.5	383	13	O42324	MU-OPIOID RECEPTOR.	1.22e-212
3	856	38.4	117	11	Q60733	OPIOID RECEPTOR, KAPPA	5.58e-113
4	643	28.8	119	11	Q64206	DELTA OPIOID RECEPTOR/	1.23e-78
5	512	23.0	263	5	O76873	EG:121E7.2 PROTEIN.	6.54e-58
6	513	23.0	387	4	O43603	GALANIN RECEPTOR GAI	4.56e-58
7	510	22.9	371	11	O88854	GALANIN RECEPTOR TYPE	1.34e-57
8	472	21.2	352	6	O77276	CHEMOKINE RECEPTOR CCR	1.13e-51
9	470	21.1	353	13	O93247	CXCR4.	2.32e-51
10	467	21.0	361	11	O35811	G-PROTEIN COUPLED RECE	6.78e-51
11	468	21.0	374	13	O57466	G PROTEIN COUPLED P2Y	4.74e-51
12	461	20.7	333	4	O14694	CCR5 RECEPTOR (FRAGMEN	5.78e-50
13	462	20.7	352	6	O18770	CCR5 RECEPTOR (FRAGMEN	4.04e-50
14	461	20.7	352	4	O15538	CCR5 RECEPTOR (FRAGMEN	5.78e-50
15	461	20.7	368	4	O60755	GALANIN 2 RECEPTOR HOM	5.78e-50
16	457	20.5	352	6	O18772	CCR5 RECEPTOR (FRAGMEN	2.41e-49
17	456	20.5	465	5	O44426	CARDIOEXCITATORY RECEP	3.44e-49
18	450	20.2	383	14	O89609	G-PROTEIN-COUPLED RECE	2.91e-48
19	449	20.1	352	6	O18771	CCR5 RECEPTOR (FRAGMEN	4.15e-48
20	448	20.1	359	11	O55169	RECEPTOR PROTEIN CKR3.	5.93e-48

21	441	19.8	359	11	O54814	CHEMOKINE RECEPTOR CCR	7.14e-47
22	442	19.8	678	5	Q94736	TACHYKININ-LIKE RECEPT	5.01e-47
23	436	19.6	353	13	P79960	MESCHENYME-ASSOCIATED	4.21e-46
24	430	19.3	357	13	O42445	CXC CHEMOKINE RECEPTOR	3.53e-45
25	431	19.3	370	11	O88853	GALANIN RECEPTOR TYPE	2.48e-45
26	429	19.2	370	11	O88626	GALANIN RECEPTOR TYPE	5.03e-45
27	425	19.1	372	13	O93237	CXC CHEMOKINE RECEPTOR	2.07e-44
28	417	18.7	367	11	O54689	G PROTEIN-COUPLED RECE	3.49e-43
29	417	18.7	370	11	O54914	GALANIN RECEPTOR TYPE	3.49e-43
30	415	18.6	238	13	Q92158	ANGIOTENSIN II RECEPTO	7.07e-43
31	415	18.6	360	6	O18793	CHEMOKINE RECEPTOR.	7.07e-43
32	415	18.6	373	11	O55193	CHEMOKINE RECEPTOR CCR	7.07e-43
33	413	18.5	399	11	O88790	BOMBESIN RECEPTOR SUBT	1.43e-42
34	413	18.5	399	11	O54798	BOMBESIN-LIKE RECEPTOR	1.43e-42
35	403	18.1	344	6	O77833	CHEMOKINE RECEPTOR CCR	4.83e-41
36	400	17.9	144	11	O08840	SOMATOSTATIN SST2B REC	1.39e-40
37	394	17.7	370	4	O15132	P2Y5-LIKE RECEPTOR.	1.14e-39
38	390	17.5	370	4	O75194	HUMAN PROLACTIN-RELEAS	4.61e-39
39	389	17.5	390	11	O54799	NEUROMEDIN B RECEPTOR.	6.55e-39
40	391	17.5	429	5	P92045	LYMNOKININ RECEPTOR.	3.25e-39
41	387	17.4	337	11	P97583	B1 BRADYKININ RECEPTOR	1.32e-38
42	378	17.0	343	11	O88537	N-FORMYLPEPTIDE RECEPT	3.05e-37
43	376	16.9	303	13	P70058	ANGIOTENSIN RECEPTOR R	6.12e-37
44	377	16.9	337	11	O35782	KININ B1 RECEPTOR.	4.32e-37
45	376	16.9	381	13	O42402	ORNITHOKININ RECEPTOR.	6.12e-37

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	373 AA.
ID	O57585;			
AC	O57585;			
DT	01-JUN-1998 (TREMREL. 05, CREATED)			
DT	01-JUN-1998 (TREMREL. 06, LAST SEQUENCE UPDATE)			
DT	01-AUG-1998 (TREMREL. 07, LAST ANNOTATION UPDATE)			
DE	OPIOID RECEPTOR HOMOLOGUE.			
OS	BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;			
OC	TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;			
OC	CYPRINIDAE; RASBORINAE; DANIO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	BARRALLO A., GONZALEZ-SARMIENTO R., GARCIA-MALVAR F., RODRIGUEZ R.E.;			
RL	SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
DR	EMBL; AJ001596; E1217996; -.			
DR	PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.			
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.			
SQ	SEQUENCE 373 AA; 42520 MW; E900D477 CRC32;			

Query Match	68.3%;	Score 1523;	DB 13;	Length 373;
Best Local Similarity	66.0%;	Pred. No. 5.90e-223;		
Matches	186;	Conservative 52;	Mismatches 40;	Indels 4; Gaps 4;
Db	80	YTKLKTATNIYIFNLALADALATSTLPFQSTKYLMTWPPGELLCKVVIADYNNMFTSI	139	
QY	1	YTKMKTATNIYIFNLALADALVTTMPFQSTVILMNSWPPFGDVLCKIVISIDYNNMFTSI	60	
Db	140	FTLTMSVDRIYIACHPVRALEFRTPKAKIINVCIIWLSSAVGVPIIMAVTRVNTQNT	199	
QY	61	FTLTMSVDRIYIACHPVKALDFRTPLKAKIINIICIIWLSSVGSIAIVLGTKVREDVD	120	
Db	200	TV-CMLKFPDPDW-YWDTVTIKICVFIFAFVVPVLVITICYGLMILRLKSVRLLSGSKEKD	257	
QY	121	VIECCQLQFPDDSYWWDLFMKICVFIFAFVIPVLIIIVCYILMILRLKXVRLLSGSREKD	180	
Db	258	RNMRRITRMVLVWVAAFIICWTPIHIFIEKTLVDINQKNPFVIASWHLHRT-GYTNSSL	316	
QY	181	XNLRRITRLVLVWVAVVVCWTPIHIFILVEALGSGSHSTA-ALSSYVFCIALGYTNSSL	239	
Db	317	NPVLYAFLDENFKRCFRDFCLPFRTRADQSNLNRATREP	358	
QY	240	NPILYAFLDENFKRCFRDFCLPKMXMERXSTSVNTVQDP	281	

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RESULT 2
ID O42324 PRELIMINARY; PRT; 383 AA.
AC O42324;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MU-OPIOID RECEPTOR.
OS CATOSTOMUS COMMERSONI (WHITE SUCKER).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
OC TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; COBITOIDEA;
OC CATOSTOMIDAE; CATOSTOMUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA DARLISON M.G., HARVEY R.J., GRETEN F.R., KREIENKAMP H.J., ZWIERS H.,
RA STHMER T., LEDERIS K., RICHTER D.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; Y10904; E1169530; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SQ SEQUENCE 383 AA; 43232 MW; 00BDBCBD CRC32;

Query Match 65.5%; Score 1451; DB 13; Length 383;
Best Local Similarity 65.1%; Pred.No. 1.22e-212;
Matches 183; Conservative 50; Mismatches 42; Indels 6; Gaps 4;

Db 85 YTKMKTATNIYIFNLADALATSTLPFSQVNYLMGTWPGDVVCKIVMSIDYNNFTSI 144
QY 1 YTKMKTATNIYIFNLADALATVTTTTPFSQSTVYLMNSWPGDVLCIVISIDYNNFTSI 60

Db 145 FTLTMSIDRYIAVCHPVKALDERTPRNAKIVNCVNWILSSAIGLPVVMVMASTTIENQNS 204
QY 61 FTLTMSVDRYIAVCHPVKALDERTPLKAKIINICIWLLSSSVGISAIVLGTKV-RED- 118

Db 205 PLQVSNFDCITLLFPPHPW-YWETLLKICVFILAFIMPVLIIVCYGLMILRLKSVRLSG 263
QY 119 -VDV--IECCLOFPDDDDYSWWDLEMKICVFIFAFVIPVLIIVCYTLMILRLKXVRLSG 175

Db 264 SKEKDRNLRRITRMVLVAVVAVFIICWTPIHIFVILKALVTIPNSLFTQVTHFICIALGYT 323
QY 176 SREKDXNLRRITRLVLVAVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFICIALGYT 235

Db 324 NSCLNPVLYAFLDENPKRCFREFCVPSVLDLQNSTRNSN 364
QY 236 NSSLNPILYAFLDENPKRCFDFCFPLKMXMERXSTSRVN 276

RESULT 3
ID Q60733 PRELIMINARY; PRT; 117 AA.
AC Q60733;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE OPIOID RECEPTOR, KAPPA 1 (KAPPA OPIOID RECEPTOR) (FRAGMENT).
GN OPRK1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA GRANDY D.K.;
RL SUBMITTED (NOV-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; U16998; G595937; -.
DR MGD; MGI:97439; OPRK1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT NON_TER 1

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FT NON_TER 117
SQ SEQUENCE 117 AA; 13070 MW; FOCF68E1 CRC32;

Query Match 38.4%; Score 856; DB 11; Length 117;
Best Local Similarity 96.6%; Pred.No. 5.58e-113;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 YTKMKTATNIYIFNLADALATVTTTTPFSQSAVYLMNSWPGDVLCIVISIGYNNFTSI 60
QY 1 YTKMKTATNIYIFNLADALATVTTTTPFSQSTVYLMNSWPGDVLCIVISIDYNNFTSI 60

Db 61 FTLTMSVDRYIAVCHPVKALDERTPLKAKIINICIWLLASSVGISAIVLGTKVRE 117
QY 61 FTLTMSVDRYIAVCHPVKALDERTPLKAKIINICIWLLSSSVGISAIVLGTKVRE 117

RESULT 4
ID Q64206 PRELIMINARY; PRT; 119 AA.
AC Q64206;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE DELTA OPIOID RECEPTOR/DOR (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96211868.
RA ROY S., SEDQI M., RAMAKRISHNAN S., BARKE R.A., LOH H.H.;
RT "Differential effects of opioids on the proliferation of a macrophage
cell line, Bac 1.2F5.";
RL CELL. IMMUNOL. 169:271-277(1996).
DR EMBL; S81965; E257299; -.
DR PFAM; PF00001; 7tm_1; 1.
FT NON_TER 1
SQ SEQUENCE 119 AA; 13380 MW; DFC85C30 CRC32;

Query Match 28.8%; Score 643; DB 11; Length 119;
Best Local Similarity 66.9%; Pred.No. 1.23e-78;
Matches 81; Conservative 18; Mismatches 19; Indels 3; Gaps 3;

Db 1 IFTLTMSVDRYIAVCHPVKALDERTPAKAKLINICIWVLASGVGPIMVMAVTPRDGA 60
QY 60 IFTLTMSVDRYIAVCHPVKALDERTPLKAKIINICIWLLSSSVGISAIVLGTKVREDV 119

Db 61 -LV-CWLQFPSPW-YWDTVTKICVFLFAFVVPVILIITVCYGLMLRLRSVRLLSGSK 117
QY 120 DVIECCLQFPDDDDYSWWDLEMKICVFIFAFVIPVLIIVCYTLMILRLKXVRLLSG 179

Db 118 D 118
QY 180 D 180

RESULT 5
ID O76873 PRELIMINARY; PRT; 263 AA.
AC O76873;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE EG:121E7.2 PROTEIN.
GN EG:121E7.2.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EFHYDROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RA MURPHY L., HARRIS D., BARRELL B.;
RT "Sequencing the distal X chromosome of Drosophila melanogaster.";
RL SUBMITTED (JUN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]

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RN [1]  
RP SEQUENCE FROM N.A.  
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,  
RA HO D.D.;  
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).  
DR EMBL; AF011536; G2305190; -.  
DR EMBL; AF011516; G2305150; -.  
DR EMBL; AF011534; G2305186; -.  
DR PFAM; PF00001; 7tm\_1; 1.  
FT NON\_TER 352 352  
SQ SEQUENCE 352 AA; 40552 MW; B1ECA8D9 CRC32;  
  
Query Match 20.7%; Score 461; DB 4; Length 352;  
Best Local Similarity 28.2%; Pred. No. 5.78e-50;  
Matches 74; Conservative 84; Mismatches 88; Indels 16; Gaps 14;  
  
Db 60 RLKSMTDIYLLNLAISDLFELLTVPE-WAHYAAAQWDFGNTMCQLLTGLYFIFGFSGIFF 118  
QY 3 KMKIATNIYIFNLADALVTTTTPFQSTVYILMNSWPFQDVLCKIVISIDYNNMFTSIPT 62  
  
Db 119 IILLTDRLAVVHAVFALKARTVTFGVTSVITWVYAVFASLPGLIFRSQ-KEGLHYT 177  
QY 63 LTMSVDRIYAVCHPVKALDERTPLKAKIINICIWLLSSSVGSAIVLGGTKVREDVDVI 122  
  
Db 178 -CSHFPYSQYQFKNFOTLKIVILGLVPLVMVICYS-GIL--KT--LLR-CRN-EKK 229  
QY 123 ECCIQFPDDYSWWDLENKICVFIFAFVIPVLIIVCYTLMILRLKXVRLLSGSREKDXN 182  
  
Db 230 RHRAVRLIFTIMIVYFELFWAPYNIIVLLNTEFQEFFGLNCCSSNRLDQAMQVTEILGMTH 289  
QY 183 LRRITRLVLVVAVFVVCWTPIHI-FIL-V-EAL-G-STSHSAALS-SYFFCIALGYTN 236  
  
Db 290 CCINPIIYAFVGEKERNYLLVF 311  
QY 237 SSLENPIIYAFLDENFKRCRDF 258

RESULT 15  
ID O60755 PRELIMINARY; PRT; 368 AA.  
AC O60755;  
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
DE GALANIN 2 RECEPTOR HOMOLOG.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
OC CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UTERUS;  
RA BENNETT M.M., LESCOE M.K., GALLIPOLI P.Z., RAMABHADHAN T.V.;  
RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 98389766.  
RA SMITH K.E., WALKER M.W., ARTYMSHYN R., BARD J., BOROWSKY B.,  
RA TAMM J.A., YAO W.-J., VAYASSE P.J.-J., BRANCHEK T.A., GERALD C.,  
RA JONES K.A.;  
RT "Cloned human and rat galanin GALR3 receptors. Pharmacology and  
RT activation of g-protein inwardly rectifying k+ channels."  
RL J. BIOL. CHEM. 273:23321-23326(1998).  
DR EMBL; AF067733; G3176927; -.  
DR EMBL; AF073799; G3608410; -.  
SQ SEQUENCE 368 AA; 39573 MW; 2DF74618 CRC32;

Query Match 20.7%; Score 461; DB 4; Length 368;  
Best Local Similarity 31.0%; Pred. No. 5.78e-50;  
Matches 88; Conservative 76; Mismatches 106; Indels 14; Gaps 10;  
  
Db 55 STTELFIINLAVADICFILCCVPFOATIYTLDAWLFALVCKAVHLLIYLTWYASFTIA 114  
QY 6 TATNIYIFNLADALA-LVTTTNPQSTVYILMNSWPFQDVLCKIVISIDYNNMFTSIPTLT 64

Db 115 AVSVDRYIAVRHPLRSALRTEFAAARAAVGL-VWLLAALFSAPILSYYGT-VR--YGALE 170  
QY 65 MMSVDRYIAVCHPVKALDERTPLKAKI-INICIWLLSSSVGISAIVLGGTKVREDVDVIE 123  
  
Db 171 LCVPAWEDA-RRRAL--DVATEAAGYLLPVAVVSLAYGRTLRLFWAAVGPAGAAAHAARR 227  
QY 124 CCLQFPDDDDYSWWDLENKICVFIFAFVIPVLIIVCY--TLMILRLKXVRLLSGSRE-KD 180  
  
Db 228 RATGRAGRAMLAVAALYALCWGPHHALIILCFWYGRFAFSPATYACRLASHCLAYANSLN 287  
QY 181 XNLRITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFFCIALGYTNSSLN 240  
  
Db 288 PLVYALASRHFRAFRRLWPCGRRRRRRHRARALRRVRPSSGPP 331  
QY 241 PILYAFLDENFKRCRDF--CFPLKMXMERXSTSRVRNTVQDPA 282

Search completed: Thu Feb 17 11:17:01 2000  
Job time : 25 secs.

GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: February 17, 2000, 09:39:05 ; Search time 66.73 Seconds  
(without alignments)  
5286.540 Million cell updates/sec  
Title: US-08-455-683-1  
Perfect score: 1410  
Sequence: 1 GCGCACCTTGCTGATCCCAA.....AACCCAGATTACAACTGCAG 1410  
Scoring table: OLIGO\_NUC  
Searched: 311585 seqs, 125096042 residues  
Database : N\_Geneseq\_36:\*  
Word size : 0  
Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1410	100.0	1410	1	Q75926	Mouse kappa opioid
2	1408	99.9	1408	1	V49254	Mouse kappa opiate
3	125	8.9	2481	1	Q86725	Mammalian kappa op
4	77	5.5	1275	1	T92601	Human kappa opioid
5	32	2.3	1000	1	Q75931	Human kappa opioid
6	32	2.3	1142	1	T12550	Human kappa opioid
7	32	2.3	1143	1	T90998	Human kappa opioid
8	32	2.3	1284	1	T90999	Human kappa opioid
9	31	2.2	2447	1	Q56702	Human kappa opioid
10	29	2.1	822	1	Q29156	Partial sequence o
11	25	1.8	1330	1	Q75928	Brain somatostatin
12	25	1.8	1567	1	Q89233	Mouse opioid recep
13	25	1.8	2600	1	Q90096	Rat opioid recepto
14	25	1.8	2706	1	Q92972	Mouse kappa-3 opio
15	25	1.8	1452	1	T89585	Rat opiorph recept
16	25	1.8	1452	1	T90381	Rat orphanin FQ re
17	25	1.8	1452	1	V56017	Rat methadone-spec
18	23	1.6	1821	1	Q56700	Sequence of murine
19	23	1.6	2216	1	Q66556	Murine delta opioi
20	23	1.6	2272	1	Q75927	Mouse delta opioid
21	23	1.6	2218	1	V49253	Mouse delta opiate
22	20	1.4	2070	1	Q79199	Rat mu-subtype opi
23	20	1.4	1618	1	Q89222	Rat mu opioid rece
24	20	1.4	1618	1	Q89223	Transcription regu
25	20	1.4	1610	1	Q89226	Human mu opioid re
26	20	1.4	2160	1	Q93102	Human mu opiate re
27	20	1.4	36	1	T12551	Human kappa opioid
28	20	1.4	39	1	T12554	Human kappa opioid
29	20	1.4	2162	1	V61985	Human mu-opioid re
30	20	1.4	2162	1	V61984	Human mu-opioid re
31	20	1.4	2162	1	V61986	Human mu-opioid re
32	20	1.4	2162	1	V61987	Human mu-opioid re
33	20	1.4	2162	1	V61988	Human mu-opioid re
34	20	1.4	2162	1	V61989	Human mu-opioid re
35	20	1.4	2162	1	V61990	Human mu-opioid re
36	20	1.4	2162	1	V61991	Human mu-opioid re
37	20	1.4	2162	1	V61992	Human mu-opioid re
38	20	1.4	2162	1	V61993	Human mu-opioid re
39	20	1.4	2162	1	V61994	Human mu-opioid re

40	20	1.4	2162	1	V61995	Human mu-opioid re
41	18	1.3	829	1	Q56703	Partial sequence o
42	18	1.3	403	1	X39521	Human secreted pro
43	17	1.2	7960	1	N90568	Ovine Y-chromosoma
44	17	1.2	11715	1	N81564	Genomic sequence e
45	17	1.2	11724	1	N70102	Complete genomic s

ALIGNMENTS

RESULT 1  
Q75926  
ID Q75926 standard; DNA; 1410 BP.  
AC Q75926;  
DT 17-AUG-1995 (first entry)  
DE Mouse kappa opioid receptor MORK1 cDNA.  
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;  
KW transmembrane domain; somatostatin; receptor; human; expression vector;  
KW truncate; chimaeric; assay; probe; ss.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT cds 186..1328  
FT /\*tag= a  
FT /product= mouse kappa opioid receptor  
PN WO9428132-A.  
PD 08-DEC-1994.  
PF 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.  
PR 30-JUL-1993; US-100594.  
PR 05-NOV-1993; US-147592.  
PA (ARCH-) ARCH DEV CORP.  
PI Bell GI, Reisine T, Yasuda K;  
DR WPI; 95-023804/03.  
DR P-PSDB; R67669.  
PT Polynucleotides and peptides derived from opioid receptor  
PT polypeptides - for use in therapeutic compositions and in  
PT screening assays for useful drug substances.  
PS Claim 10; Page 207-211; 300pp; English.  
CC The nucleotide sequence of the novel mouse kappa opioid receptor gene  
CC MORK1. The gene was isolated from a mouse brain cDNA library using a  
CC fragment (amplified from the cDNA library with primers Q75929-30) as a  
CC probe. The primers are based on the conserved sequences present in the  
CC second and third transmembrane domains of somatostatin (SRIF) receptor  
CC subtypes SST1, SST2 and SST3. The 1.2 kb PSTI fragment from the mouse  
CC kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV  
CC promoter-based expression vector pCMV-6b. The resultant construct  
CC pCMV-msl-1 was transfected into COS-1 cells for protein production. The  
CC gene encoding the opioid receptor can be used to produce complete,  
CC truncated or chimaeric opioid receptor proteins. The opioid receptors  
CC thus produced are useful for the development of novel assays designed to  
CC select or improve substances, capable of interacting with the opioid  
CC receptor proteins, for use in diagnosis, drug design and therapeutic  
CC applications.  
SQ Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T;

Query Match 100.0%; Score 1410; DB 1; Length 1410;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCGCACCTTGCTGATCCCAAACAGGCAGAGCTTCTTCCAGTCTTGGAGGCACAAATTGA	60
Db	1	GCGCACCTTGCTGATCCCAAACAGGCAGAGCTTCTTCCAGTCTTGGAGGCACAAATTGA	60
QY	61	GCATCAGGAACGTGGACCCCATCAGGGCTGAACAGCTACTCAGGATCTAAAGTGGTACTT	120
Db	61	GCATCAGGAACGTGGACCCCATCAGGGCTGAACAGCTACTCAGGATCTAAAGTGGTACTT	120
QY	121	GGAAGCTGACGGTGACITGGGAAGGGAGGTGCGCCATCAGGATCTGGAGCTGAGCGC	180
Db	121	GGAAGCTGACGGTGACITGGGAAGGGAGGTGCGCCATCAGGATCTGGAGCTGAGCGC	180

QY 181 TCACCATGGAGTCCGCCAATTCAGATCTTCCGAGGAGATCCAGGCCCTACCTGCTCTCCCA 240  
Db 181 TCACCATGGAGTCCGCCAATTCAGATCTTCCGAGGAGATCCAGGCCCTACCTGCTCTCCCA 240  
QY 241 GTGCTTGCTTCTCCCAACAGCAGCTCTTGGTTCGCCAACTGGGCAGAAATCCGACAGTA 300  
Db 241 GTGCTTGCTTCTCCCAACAGCAGCTCTTGGTTCGCCAACTGGGCAGAAATCCGACAGTA 300  
QY 301 ATGGCAGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGGCCACATCTCTCCGGCCATCC 360  
Db 301 ATGGCAGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGGCCACATCTCTCCGGCCATCC 360  
QY 361 CTGTTATCATCACCGCTGTCTACTCTGTGGTATTTGGTGGGCTTAGTGGCAATCTC 420  
Db 361 CTGTTATCATCACCGCTGTCTACTCTGTGGTATTTGGTGGGCTTAGTGGCAATCTC 420  
QY 421 TGGTCATGTTTGTCTATCATCCGATACACGAAGATGAAGACCGCAACCAACATCTACATAT 480  
Db 421 TGGTCATGTTTGTCTATCATCCGATACACGAAGATGAAGACCGCAACCAACATCTACATAT 480  
QY 481 TTAACCTGGCTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTTCAGAGTGTGTCT 540  
Db 481 TTAACCTGGCTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTTCAGAGTGTGTCT 540  
QY 541 ACTTGATGAATTTCTTGGCCTTTTGGAGATGTGCTATGCAAGATTGTCTATTTCCATTGACT 600  
Db 541 ACTTGATGAATTTCTTGGCCTTTTGGAGATGTGCTATGCAAGATTGTCTATTTCCATTGACT 600  
QY 601 ACTACAACATGTTTACCAGCATATTTCCCTTGACCATGATGATGATGATGATGATGATG 660  
Db 601 ACTACAACATGTTTACCAGCATATTTCCCTTGACCATGATGATGATGATGATGATGATG 660  
QY 661 CTGTGTGCCACCCCTGTGAAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAAAGATCATCA 720  
Db 661 CTGTGTGCCACCCCTGTGAAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAAAGATCATCA 720  
QY 721 ACATCTGCATTTGGCTCCTTGGCATCATCTGTTGGTATATCAGCGATAGTCTTGGAGGCA 780  
Db 721 ACATCTGCATTTGGCTCCTTGGCATCATCTGTTGGTATATCAGCGATAGTCTTGGAGGCA 780  
QY 781 CCAAAGTCAGGAAGATGTGGATGTCTATGATGCTCTTCCCTGCAGTTTCCCTGATGATGAAT 840  
Db 781 CCAAAGTCAGGAAGATGTGGATGTCTATGATGCTCTTCCCTGCAGTTTCCCTGATGATGAAT 840  
QY 841 AATCCTGGTGGGATCTCTTCAATGAAGATCTGTGCTCTTGGTCTTGGCTTTGTGATCCAG 900  
Db 841 AATCCTGGTGGGATCTCTTCAATGAAGATCTGTGCTCTTGGTCTTGGCTTTGTGATCCAG 900  
QY 901 TCCTCATCATCATTTGTCTGCTACACCTGTATGATCTCGGCTTGAAGAGTGTCCGGCTCC 960  
Db 901 TCCTCATCATCATTTGTCTGCTACACCTGTATGATCTCGGCTTGAAGAGTGTCCGGCTCC 960  
QY 961 TGTCTGGCTCCGAGAGAGGACCGAATCTCCGCCATCACCAGCTGGTCTGGTAG 1020  
Db 961 TGTCTGGCTCCGAGAGAGGACCGAATCTCCGCCATCACCAGCTGGTCTGGTAG 1020  
QY 1021 TAGTTGCAGTCTTCATCATCTGTTGGACCCCATTCACATCTTTATCTCTGATGCTCTGG 1080  
Db 1021 TAGTTGCAGTCTTCATCATCTGTTGGACCCCATTCACATCTTTATCTCTGATGCTCTGG 1080  
QY 1081 TGGGAAGCACTCCACAGACAGCTGCCCTTCCAGCTATTATTTCTGATGCTCTGG 1140  
Db 1081 TGGGAAGCACTCCACAGACAGCTGCCCTTCCAGCTATTATTTCTGATGCTCTGG 1140  
QY 1141 GTTATACCAACAGAGCCTGAAATCCTGTTTCTCTATGCCCTTCTGGATGAAACCTCAAGC 1200  
Db 1141 GTTATACCAACAGAGCCTGAAATCCTGTTTCTCTATGCCCTTCTGGATGAAACCTCAAGC 1200  
QY 1201 GGTGTTTTAGGGACTTCTGCTTCCCTATTAAAGATGCGAATGGAGCGCCAGACCAATA 1260  
Db 1201 GGTGTTTTAGGGACTTCTGCTTCCCTATTAAAGATGCGAATGGAGCGCCAGACCAATA 1260  
QY 1261 GAGTTAGAAACACAGTTTCAGGATCTGCTTCCATGAGAGTGTGGAGGGATGATAAAGC 1320

Db 1261 GAGTTAGAAACACAGTTCAGGATCCIGCTTCCATGAGAGATGTGGGAGGATGAATAAGC 1320  
QY 1321 CAGTATGACTAGTGTGAAATGTCTTCTTATTTCTCCAGGTAGAGAAGAGTTCAATG 1380  
Db 1321 CAGTATGACTAGTGTGAAATGTCTTCTTATTTCTCCAGGTAGAGAAGAGTTCAATG 1380  
QY 1381 ATCTTGGTTTAAACCCAGATTACAACTGCAG 1410  
Db 1381 ATCTTGGTTTAAACCCAGATTACAACTGCAG 1410  
RESULT 2  
V49254  
ID V49254 standard; DNA; 1408 BP.  
AC V49254;  
DI 28-OCT-1998 (first entry)  
DE Mouse kappa opiate receptor gene.  
KW Mouse; kappa opiate receptor; transgenic animal; mammal; identification;  
KW exon; nervous tissue; pain; drug addiction; transplant rejection;  
KW immunosuppressant; analgesic; morphine; side effect; ds.  
OS Mus sp.  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 184..1326  
FT /\*tag= a  
FT /product= "kappa opiate receptor"  
W09802534-A2.  
PN 22-JAN-1998.  
PF 11-JUL-1997; F01282.  
PR 15-JUL-1996; FR-008810.  
PA (CNRS ) CENT NAT RECH SCI.  
PI Dierich A, Kieffer BL, LeMeur M, Matthes HWD, Simonin FH;  
DR WPI; 98-110582/10.  
DR P-PSDB; W44939.  
PT Transgenic animals defective in one type of opiod receptor - used  
PT to identify agents for treatment of pain, drug addiction and  
PT transplant rejection, lacking side effects of known opiate(s)  
PT  
PS Disclosure; Fig 13; 58pp; French.  
CC This sequence represents the gene encoding the mouse kappa opiate  
CC receptor protein. The sequence is used to generate a transgenic  
CC non-human mammal for identifying agents for treating disorders  
CC associated with opiate receptors. In the mammal, the expression of  
CC the gene encoding the opiate receptor is modified, particularly by  
CC the deletion of an exon and/or insertion of a marker gene, e.g. the  
CC neomycin resistance gene, into the sequence. Especially the expression  
CC of the gene is altered in nervous tissue. The agents are potentially  
CC useful for treating severe pain (chronic or acute), drug addiction and/or  
CC prevention or treatment of transplant rejection (as immunosuppressants).  
CC The method may isolate and identify powerful analgesics that lack  
CC morphine-like side effects.  
CC Sequence 1408 BP; 322 A; 359 C; 336 G; 391 T;  
SQ

Query Match 99.9%; Score 1408; DB 1; Length 1408;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCACCTTGTGATCCCAACAGGAGAGCTTCTCCAGTCTTGGAGGCACAAATTGAGC 62  
Db 1 GCACCTTGTGATCCCAACAGGAGAGCTTCTCCAGTCTTGGAGGCACAAATTGAGC 60  
QY 63 ATCAGGAACGTGGACCCCATCAGGGCTGAACAGCTACTCAGGATCTAAAGTGGTACTGG 122  
Db 61 ATCAGGAACGTGGACCCCATCAGGGCTGAACAGCTACTCAGGATCTAAAGTGGTACTGG 120  
QY 123 AAAGCTGACGGTACTTGGGAAGGAGGTGCGCAATCAGCGATCTGGAGTGCAGCGCTC 182  
Db 121 AAAGCTGACGGTACTTGGGAAGGAGGTGCGCAATCAGCGATCTGGAGTGCAGCGCTC 180  
QY 183 ACCATGGAGTCCCCCATTCAGATCTTCCGAGGAGATCCAGGCCCTACCTGCTCTCCAGT 242  
Db 181 ACCATGGAGTCCCCCATTCAGATCTTCCGAGGAGATCCAGGCCCTACCTGCTCTCCAGT 240

QY	243	GC	TTGGCTTC	CCCCAACAGCAGCCTCTTGGTCCCCAACTGGCAGAAATCCGACAGTAAT	300
DB	241	GC	TGGCTTCT	CCCCAACAGCAGCCTCTTGGTCCCCAACTGGCAGAAATCCGACAGTAAT	300
QY	303	GG	CAGTGTGG	CTCAGAGGATCAGCAGCTGGAGTCCGGCAGCATCTCTCCGGCCATCCCT	362
DB	301	GG	CAGTGTGG	CTCAGAGGATCAGCAGCTGGAGTCCGGCAGCATCTCTCCGGCCATCCCT	360
QY	363	GT	TATCATCACCGCTGTCTACTCTGTGGTATTGTGGTGGCTTAGTGGCAATTCTCTG	422	
DB	361	GT	TATCATCACCGCTGTCTACTCTGTGGTATTGTGGTGGCTTAGTGGCAATTCTCTG	420	
QY	423	GTCATGTTTGTCATCATCCGATACACGAAGATGAAGACCCGCAACCAATCTACATAATT	482		
DB	421	GTCATGTTTGTCATCATCCGATACACGAAGATGAAGACCCGCAACCAATCTACATAATT	480		
QY	483	AACCTGGCTTTTGGCAGATGCTTTGGTTACTACCACATATGCCCTTTCAGAGTGTGTCTAC	542		
DB	481	AACCTGGCTTTTGGCAGATGCTTTGGTTACTACCACATATGCCCTTTCAGAGTGTGTCTAC	540		
QY	543	TTGATGAATTCTTGGCCCTTTTGGAGATGTGCTATGCAAGATGTCTATTTCCATTGACTAC	602		
DB	541	TTGATGAATTCTTGGCCCTTTTGGAGATGTGCTATGCAAGATGTCTATTTCCATTGACTAC	600		
QY	603	TACAACATGTTTACCAGCATATTACCTTGACCATGATGAGTGTGGACCGCTACATTGCT	662		
DB	601	TACAACATGTTTACCAGCATATTACCTTGACCATGATGAGTGTGGACCGCTACATTGCT	660		
QY	663	GTTGGCCACCTGTGAAAGCTTTGGACTTCGAAACACCTTTGAAAGCAAAGATCATCAAC	722		
DB	661	GTTGGCCACCTGTGAAAGCTTTGGACTTCGAAACACCTTTGAAAGCAAAGATCATCAAC	720		
QY	723	ATCTGCATTTGGCTCCTGGCATCATCTGTTGGTATATCAGCGATAGTCTCTGGAGGCACC	782		
DB	721	ATCTGCATTTGGCTCCTGGCATCATCTGTTGGTATATCAGCGATAGTCTCTGGAGGCACC	780		
QY	783	AAAGTCAGGGAAGATGTGGATGTCATTGAATGCTCCTTGCAGTTTCTGTGATGATGAAT	842		
DB	781	AAAGTCAGGGAAGATGTGGATGTCATTGAATGCTCCTTGCAGTTTCTGTGATGATGAAT	840		
QY	843	TCCTGGTGGATCTCTTCATGAAGATCTGTGTTTGGTCTTTCGCTTTGTGATCCCAGTC	902		
DB	841	TCCTGGTGGATCTCTTCATGAAGATCTGTGTTTGGTCTTTCGCTTTGTGATCCCAGTC	900		
QY	903	CTCATCATATTGTGTGCTACACCCCTGATGATCCTCGCCGATCACCAGCTGGTGTGGTAGTA	962		
DB	901	CTCATCATATTGTGTGCTACACCCCTGATGATCCTCGCCGATCACCAGCTGGTGTGGTAGTA	960		
QY	963	TC	TGGCTCCGAGAGAAAGACCGAAATCTCCGCCGATCACCAGCTGGTGTGGTAGTA	1022	
DB	961	TC	TGGCTCCGAGAGAAAGACCGAAATCTCCGCCGATCACCAGCTGGTGTGGTAGTA	1020	
QY	1023	GTTG	CAGTCTTCATCATCTGTGGACCCCATTCATCTTATCCTGGTGGAGGCTGTG	1082	
DB	1021	GTTG	CAGTCTTCATCATCTGTGGACCCCATTCATCTTATCCTGGTGGAGGCTGTG	1080	
QY	1083	GG	AAGCACCTCCCACAGCACAGCTGCCCTCTCCAGCTATTATTTCTGTATTCCCTTGGGT	1142	
DB	1081	GGA	GCACCTCCCACAGCACAGCTGCCCTCTCCAGCTATTATTTCTGTATTCCCTTGGGT	1140	
QY	1143	TAT	ACCAACAGCAGCCCTGAATCCTGTCTCTATGCCCTTCTGGATGAAACTTCAAGCGG	1202	
DB	1141	TAT	ACCAACAGCAGCCCTGAATCCTGTCTCTATGCCCTTCTGGATGAAACTTCAAGCGG	1200	
QY	1203	TG	TTTAGGGACTTCTGCTTCCCTATTAAAGATCGGAATGGAGCGCAGACCAATAGA	1262	
DB	1201	TG	TTTAGGGACTTCTGCTTCCCTATTAAAGATCGGAATGGAGCGCAGACCAATAGA	1260	
QY	1263	GTT	AGAAACACAGTTCAGGATCCTGCTTCCATGAGAGATGTGGAGGGATGAATAAGCCA	1322	
DB	1261	GTT	AGAAACACAGTTCAGGATCCTGCTTCCATGAGAGATGTGGAGGGATGAATAAGCCA	1320	
QY	1323	GI	ATGACTAGTCGTGGAAATGTCTTCTTATTTCTCCAGTATGAGAGAGTTCAATGAT	1382	

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||||| 1321 GTATGACTAGTCCGTGGAAATGTCTTCTTATTGTTCTCTCCAGGTAGAGAAGAGTTCAATGAT 1380
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QY 1383 CTTGGTTTAACCCAGATTACAACTGCAG 1410
|||||
Db 1381 CTTGGTTTAACCCAGATTACAACTGCAG 1408
|||||

RESULT 3
Q86725
ID Q86725 standard; cDNA; 2481 BP.
AC Q86725;
DT 01-DEC-1995 (first entry)
DE Mammalian kappa opioid receptor protein cDNA.
KW Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;
KW amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
OS Rattus rattus.
FH Key
FT cds
FT 111..1253
FT /*tag= a
FT /product= kappa opioid receptor
PN J07070191-A.
PD 14-MAR-1995.
PF 30-JUL-1993; 190261.
PR 09-JUL-1993; JP-170591.
PA (TAKE ) TAKEDA CHEM IND LTD.
DR WPI; 95-144857/19.
DR P-PSDB; R72591.
PT Kappa opioid receptor protein and cells expressing it - useful
PT for the screening of compounds for analgesic and hypnotic
PT properties
PS Claim 2; Page 9-10; 15pp; Japanese.
CC The publ. no. 1995-01-12

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RESULT	4
T92601	
ID	T92601 standard; cDNA; 1275 bp.

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AC T92601;
DT 14-APR-1998 (first entry)
DE Human kappa opioid receptor prototype RASSL OR1 DNA.
KW Selective target cell activation; G protein-coupled receptor;
KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;
KW human; transgenic animal; arrhythmia; bone disease; seizure;
KW vascular contraction; disease model; ss.
OS Chimeric - Homo sapiens.
OS Chimeric - Synthetic.
FH Key Location/Qualifiers
FT sig_peptide 1..90
/*tag= a prolactin signal sequence
/*product=
91..1284
FT mat_peptide /*tag= b
/*product= FLAG-modified KOR-HA fusion
FT misc_feature 702..787
/*tag= c
/*note= "delta opioid receptor sequence"
FT FT
PN WO9735478-A1.
PD 02-OCT-1997.
PF 25-MAR-1997; U05334.
PR 26-MAR-1996; US-622348.
PA (REGC ) UNIV CALIFORNIA.
PI Conklin BR;
DR WPI; 97-502739/46.
DR P-PSDB; W30299.
DR Selective activation of target cell expressing modified G protein
PT coupled receptor - allows control of cellular proliferation,
PT especially for amplification of transfected cells in gene therapy
PT Example 1; Page 80-82; 117pp; English.
PS This cDNA sequence encodes RASSL OR1 (see W30299) a G protein-
CC coupled receptor that is activated superiorly by synthetic ligands.
CC OR1 comprises human G protein-coupled kappa opioid receptor (KOR)
CC (see also W30297) modified at 17 amino acid positions to contain
CC the corresponding amino acid of the delta opioid receptor. The OR1
CC polynucleotide was obtained by site-directed mutagenesis of native
CC human KOR cDNA (see T90998) and includes flanking sequences that
CC encode signal and epitope peptides to facilitate the detection and
CC purification of recombinant OR1. A novel method for selectively
CC activating a target cell (TC) comprises: (i) introducing into the
CC cell a nucleic acid sequence (I) that expresses a RASSL (A) and
CC (ii) exposing the transfected cell to small synthetic molecules
CC (B) that bind to and activate (A), inducing the G protein coupled
CC cellular response associated with receptor activation. (A) has: (a)
CC decreased binding affinity for a selected natural ligand of the
CC native receptor; (b) binding affinity for (B); and (c) is activated
CC by binding (B) sufficiently to produce the required cellular response.
CC Also new are: transgenic cells including heterologous (I) in the
CC genome; cellular implants comprising a TC transfected with (I);
CC isolated (I); and transgenic animals expressing (A). Activation, or
CC (A) results, in vitro or in vivo, in cellular proliferation, or
CC secretion of a cellular product, particularly a heterologous
CC therapeutic protein encoded by a second inserted nucleic acid
CC sequence. Particularly it is used to expand the relatively few
CC cells that are successfully transfected during gene therapy
CC procedures. Other responses that can be regulated are cell
CC migration and contraction, or pigment production. In transgenic
CC animals, expression or stimulation of (A) is designed to develop
CC cardiac arrhythmia, symptoms of bone disease, seizures, vascular
CC contractions, dementia, neurodegeneration etc., for use as models
CC of these diseases (claimed). The transgenic animals are also used
CC for production of improved food products (e.g. increased calcium
CC content in eggshells or altered fat/lean ratios) or to control
CC fertility or induce labour.
CC Sequence 1275 BP; 265 A; 373 C; 318 G; 318 T;
SQ

Query Match 5.5%; Score 77; DB 1; Length 1275;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 TGCAAGATTGTCATTTCCTGACTACTACACATGTTTACCAGCATATTCACCTTGACC 635

AC T92601;
DT 14-APR-1998 (first entry)
DE Human kappa opioid receptor prototype RASSL OR1 DNA.
KW Selective target cell activation; G protein-coupled receptor;
KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;
KW human; transgenic animal; arrhythmia; bone disease; seizure;
KW vascular contraction; disease model; ss.
OS Chimeric - Homo sapiens.
OS Chimeric - Synthetic.
FH Key Location/Qualifiers
FT sig_peptide 1..90
/*tag= a prolactin signal sequence
/*product=
91..1284
FT mat_peptide /*tag= b
/*product= FLAG-modified KOR-HA fusion
FT misc_feature 702..787
/*tag= c
/*note= "delta opioid receptor sequence"
FT FT
PN WO9735478-A1.
PD 02-OCT-1997.
PF 25-MAR-1997; U05334.
PR 26-MAR-1996; US-622348.
PA (REGC ) UNIV CALIFORNIA.
PI Conklin BR;
DR WPI; 97-502739/46.
DR P-PSDB; W30299.
DR Selective activation of target cell expressing modified G protein
PT coupled receptor - allows control of cellular proliferation,
PT especially for amplification of transfected cells in gene therapy
PT Example 1; Page 80-82; 117pp; English.
PS This cDNA sequence encodes RASSL OR1 (see W30299) a G protein-
CC coupled receptor that is activated superiorly by synthetic ligands.
CC OR1 comprises human G protein-coupled kappa opioid receptor (KOR)
CC (see also W30297) modified at 17 amino acid positions to contain
CC the corresponding amino acid of the delta opioid receptor. The OR1
CC polynucleotide was obtained by site-directed mutagenesis of native
CC human KOR cDNA (see T90998) and includes flanking sequences that
CC encode signal and epitope peptides to facilitate the detection and
CC purification of recombinant OR1. A novel method for selectively
CC activating a target cell (TC) comprises: (i) introducing into the
CC cell a nucleic acid sequence (I) that expresses a RASSL (A) and
CC (ii) exposing the transfected cell to small synthetic molecules
CC (B) that bind to and activate (A), inducing the G protein coupled
CC cellular response associated with receptor activation. (A) has: (a)
CC decreased binding affinity for a selected natural ligand of the
CC native receptor; (b) binding affinity for (B); and (c) is activated
CC by binding (B) sufficiently to produce the required cellular response.
CC Also new are: transgenic cells including heterologous (I) in the
CC genome; cellular implants comprising a TC transfected with (I);
CC isolated (I); and transgenic animals expressing (A). Activation, or
CC (A) results, in vitro or in vivo, in cellular proliferation, or
CC secretion of a cellular product, particularly a heterologous
CC therapeutic protein encoded by a second inserted nucleic acid
CC sequence. Particularly it is used to expand the relatively few
CC cells that are successfully transfected during gene therapy
CC procedures. Other responses that can be regulated are cell
CC migration and contraction, or pigment production. In transgenic
CC animals, expression or stimulation of (A) is designed to develop
CC cardiac arrhythmia, symptoms of bone disease, seizures, vascular
CC contractions, dementia, neurodegeneration etc., for use as models
CC of these diseases (claimed). The transgenic animals are also used
CC for production of improved food products (e.g. increased calcium
CC content in eggshells or altered fat/lean ratios) or to control
CC fertility or induce labour.
CC Sequence 1275 BP; 265 A; 373 C; 318 G; 318 T;
SQ

Query Match 5.5%; Score 77; DB 1; Length 1275;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 TGCAAGATTGTCATTTCCTGACTACTACACATGTTTACCAGCATATTCACCTTGACC 635

DB 502 TGCAAGATTGTCATTTCCTGACTACTACACATGTTTACCAGCATATTCACCTTGACC 561
QY 636 ATGATGAGTGTGGACCG 652
DB 562 ATGATGAGTGTGGACCG 578

RESULT 5
Q75931
ID Q75931 standard; DNA; 1000 BP.
AC Q75931;
DT 18-AUG-1995 (first entry)
DE Human kappa opioid receptor partial cDNA fragment.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Key 102..989
/*tag= a
/*product= partial human kappa opioid receptor
FT FT
PN WO9428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR P-PSDB; R67672.
DR Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 10; Page 236-239; 300pp; English.
CC The partial nucleotide sequence of the novel human kappa opioid receptor
CC gene. The gene was isolated from a human brain hippocampus cDNA library
CC using a probe from the mouse kappa opioid receptor gene (Q75926). The
CC gene is missing the N-terminal sequence. The C-terminal sequence is
CC very similar to the mouse kappa opioid receptor sequence. Of the
CC C-terminal 293 amino acids, 281 residues are identical and 6 residues
CC have conservative substitutions. The gene encoding the human opioid
CC receptor can be placed in a suitable expression vector for production of
CC the protein in a cell. The opioid receptors thus produced are useful for
CC the development of novel assays designed to select or improve substances,
CC capable of interacting with the opioid receptor proteins, for use in
CC diagnosis, drug design and therapeutic applications. 278 T;
SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 225 T;

Query Match 2.3%; Score 32; DB 1; Length 1000;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 TACATATTTAACCTGGCTTTGGCAGATGCTTT 505
DB 132 TACATATTTAACCTGGCTTTGGCAGATGCTTT 163

RESULT 6
T12550
ID T12550 standard; cDNA; 1142 BP.
AC T12550;
DT 03-SEP-1996 (first entry)
DE Human kappa opioid receptor cDNA.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Key 1..1142
/*tag= a
/*product= kappa_opioid_receptor
FT FT
```

FT WO9601898-A1. /note= "incomplete termination codon"

PN 25-JAN-1996.

PD 07-JUL-1995; F00912.

PF 11-JUL-1994; FR-008531.

PR (UYST-) UNIV PASTEUR STRASBOURG LOUIS.

PA Kieffer B, Simonin F;

PI WPI; 96-097628/10.

DR P-PSDB; R88722.

DR New nucleic acid encoding the human Kappa opioid receptor - useful

PT in diagnosis and therapy, and for isolating receptor ligands and

PT modulators

PS Claim 3; Page 13-15; 30pp; French.

CC This sequence codes for the human kappa opioid receptor and was

CC obtained from two overlapping cDNA fragments isolated from a

CC human placental cDNA library. The fragments were amplified from

CC the library using PCR primers based on the sequence of human

CC genomic clones which hybridised with a murine delta receptor cDNA

CC probe. Nucleotide probes derived from the kappa opioid receptor

CC coding sequence are useful for diagnosis of neurological, cardio-

CC vascular and psychiatric disorders associated with opioid

CC receptors.

SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

Query Match 2.3%; Score 32; DB 1; Length 1142;

Best Local Similarity 100.0%; Pred. No. 2e-06;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 TACATATTAACTGGCTTTGGCAGATGCTTT 505

Db 289 TACATATTAACTGGCTTTGGCAGATGCTTT 320

RESULT 7

T90998

ID T90998 standard; cDNA; 1143 BP.

AC T90998;

DT 14-APR-1998 (first entry)

DE Human kappa opioid receptor cDNA.

KW Selective target cell activation; G protein-coupled receptor;

KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;

KW human; transgenic animal; arrhythmia; bone disease; seizure;

KW vascular contraction; disease model; ss.

OS Homo sapiens.

PN WO9735478-A1.

PD 02-OCT-1997.

PF 25-MAR-1997; U05334.

PR 26-MAR-1996; US-622348.

PA (REGC ) UNIV CALIFORNIA.

PI Conklin BR;

DR WPI; 97-502739/46.

DR P-PSDB; W30297.

PT Selective activation of target cell expressing modified G protein

PT coupled receptor - allows control of cellular proliferation,

PT especially for amplification of transfected cells in gene therapy

PS Example 1; Page 74-76; 117pp; English.

CC This cDNA sequence comprises the coding region for human kappa

CC opioid receptor (KOR, see W30297), a G protein-coupled receptor

CC implicated in neurotransmission. A novel method for selectively

CC activating a target cell (TC) comprises: (i) introducing into the

CC cell a nucleic acid sequence (I) that expresses a G protein-coupled

CC receptor (A) modified to be activated superiorly by a synthetic

CC ligand (RASSL); and (ii) exposing the transfected cell to small

CC synthetic molecules (B) that bind to and activate (A), inducing the

CC G protein coupled cellular response associated with receptor

CC activation. (A) has: (a) decreased binding affinity for a selected

CC natural ligand of the native receptor; (b) binding affinity for

CC (B); and (c) is activated by binding (B) sufficiently to produce

CC the required cellular response. Also new are: (1) transgenic cells

CC including heterologous (I) in the genome; (2) cellular implants

CC comprising a TC transfected with (I); (3) isolated (I); and (4)

CC transgenic non-human animals expressing (A). Activation of (A)

CC results, in vitro or in vivo, in cellular proliferation, or

CC secretion of a cellular product, particularly a heterologous

CC therapeutic protein encoded by a second inserted nucleic acid

CC sequence. Particularly it is used to expand the relatively few

CC cells that are successfully transfected during gene therapy

CC procedures. Other responses that can be regulated are cell

CC migration and contraction, or pigment production. In transgenic

CC animals, expression or stimulation of (A) is designed to develop

CC cardiac arrhythmia, symptoms of bone disease, seizures, vascular

CC contractions, dementia, neurodegeneration etc., for use as models

CC of these diseases (claimed). The transgenic animals are also used

CC for production of improved food products (e.g. increased calcium

CC content in eggshells or altered fat/lean ratios) or to control

CC fertility or induce labour. A RASSL derived from KOR, designated

CC RASSL OR1 (see W30299), was generated by mutation of the KOR

CC cDNA sequence.

SQ Sequence 1143 BP; 237 A; 337 C; 283 G; 286 T;

Query Match 2.3%; Score 32; DB 1; Length 1143;

Best Local Similarity 100.0%; Pred. No. 2e-06;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 TACATATTAACTGGCTTTGGCAGATGCTTT 505

Db 289 TACATATTAACTGGCTTTGGCAGATGCTTT 320

RESULT 8

T90999

ID T90999 standard; cDNA; 1284 BP.

AC T90999;

DT 14-APR-1998 (first entry)

DE Human kappa opioid receptor modified cDNA.

KW Selective target cell activation; G protein-coupled receptor;

KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;

KW human; transgenic animal; arrhythmia; bone disease; seizure;

KW vascular contraction; disease model; ss.

OS Chimeric - Homo sapiens.

PN WO9735478-A1.

PD 02-OCT-1997.

PF 25-MAR-1997; U05334.

PR 26-MAR-1996; US-622348.

PA (REGC ) UNIV CALIFORNIA.

PI Conklin BR;

DR WPI; 97-502739/46.

DR P-PSDB; W30298.

PT Selective activation of target cell expressing modified G protein

PT coupled receptor - allows control of cellular proliferation,

PT especially for amplification of transfected cells in gene therapy

PS Example 1; Page 77-79; 117pp; English.

CC This cDNA sequence encodes a polypeptide (see W30298) comprising

CC the human G protein-coupled kappa opioid receptor (KOR) (see also

CC W30297) flanked by sequences that facilitate the detection and

CC purification of recombinant KOR, and especially KOR RASSLs (see

CC W30299), i.e. a receptor activated superiorly by a synthetic

CC ligand. A novel method for selectively activating a target cell

CC (TC) comprises: (i) introducing into the cell a nucleic acid

CC sequence (I) that expresses a RASSL (A) and (ii) exposing the

CC transfected cell to small synthetic molecules (B) that bind to and

CC activate (A), inducing the G protein coupled cellular response

CC associated with receptor activation. (A) has: (a) decreased binding

CC affinity for a selected natural ligand of the native receptor; (b)

CC binding affinity for (B); and (c) is activated by binding (B)

CC sufficiently to produce the required cellular response. Also new

```
CC are: transgenic cells including heterologous (I) in the genome;
CC cellular implants comprising a TC transfected with (I); isolated
CC (I); and transgenic animals expressing (A). Activation of (A)
CC results, in vitro or in vivo, in cellular proliferation, or
CC secretion of a cellular product, particularly a heterologous
CC therapeutic protein encoded by a second inserted nucleic acid
CC sequence. Particularly it is used to expand the relatively few
CC cells that are successfully transfected during gene therapy
CC procedures. Other responses that can be regulated are cell
CC migration and contraction, or pigment production. In transgenic
CC animals, expression or stimulation of (A) is designed to develop
CC cardiac arrhythmia, symptoms of bone disease, seizures, vascular
CC contractions, dementia, neurodegeneration etc., for use as models
CC of these diseases (claimed). The transgenic animals are also used
CC for production of improved food products (e.g. increased calcium
CC content in eggshells or altered fat/lean ratios) or to control
CC fertility or induce labour.
SQ Sequence 1284 BP; 265 A; 377 C; 322 G; 320 T;

Query Match 2.3%; Score 32; DB 1; Length 1284;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 TACATATTAACTGGCTTTGGCAGATGCTTT 505
|||||
Db 400 TACATATTAACTGGCTTTGGCAGATGCTTT 431

RESULT 9
Q56702
ID Q56702 standard; DNA; 2447 BP.
AC Q56702;
DT 15-SEP-1994 (first entry)
DE Partial sequence of the human kappa opioid receptor
DE genomic clone H14 (KORa).
KW Opioid receptor; morphine; opiate; ss.
OS Homo sapiens.
PN WO9404552-A.
PD 03-MAR-1994.
PF 13-AUG-1993; U07665.
PR 13-AUG-1992; US-929200.
PA (REGC ) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
DR WPI; 94-083099/10.
PT DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpds. for opioid (ant)agonist activity
PS Example; Fig 8b; 74pp; English.
CC To isolate opiate receptor genomic clones, 300,000 human genomic
CC clones and a similar number of mouse genomic clones were probed
CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI
CC fragment. One mouse clone and three human genomic clones were
CC isolated. The 3 human clones had very different EcoRI patterns
CC which indicated that three different genes were represented by the
CC human genomic clones which were designated H3, H14 and H20. H14 maps
CC to chromosome 8. It encodes the human kappa opioid receptor.
SQ Sequence 2447 BP; 683 A; 512 C; 498 G; 747 T;

Query Match 2.2%; Score 31; DB 1; Length 2447;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 ATAGTCCTTGGAGGCACCAAGTCAGGGAAG 795
|||||
Db 213 ATAGTCCTTGGAGGCACCAAGTCAGGGAAG 243

RESULT 10
Q29156
ID Q29156 standard; DNA; 822 BP.
AC Q29156;
```

```
DT 08-MAR-1993 (first entry)
DE Brain somatostatin receptor 5' DNA.
KW SR; antibodies; tumours; glycoprotein; pancreatic somatostatinoma;
KW rat; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT Key 1..822
FT cds /*tag= a
PN EP-508221-A.
PD 14-OCT-1992.
PF 25-MAR-1992; 105164.
PR 28-MAR-1991; US-677009.
PR 07-JAN-1992; US-817921.
PA (AMCY ) AMERICAN CYANAMID CO.
PI Corbett MJ, Eppler CM, Hadcock J, Hulmes JD, Shieh H;
PI Strnad J, Zyskjr, Cecil ME;
PI WPI; 92-341551/42.
DR P-PSDB; R27505.
DR New somatostatin receptor, active fragments and antibodies -
PT prevents somatostatin binding to its receptor, useful for
PT treating and detecting tumours e.g. pancreatic somatostatinoma
PT Claim 18; Fig 10; 50pp; English.
PS A partial clone of purified pituitary somatostatin was used to design
CC PCR primers for amplification of somatostatin receptor DNA i.e.
CC primers ICII and TM VII. Rat genomic DNA was subjected to PCR and
CC from the deduced location of the corresp. peptides i.e. TM VII and
CC ICII, a 501 bp fragment of the receptor cDNA was obtd. This sequence
CC was used in PCR to obtain the 5' rat brain SR sequence (some bases
CC undefined and having a gap in the sequence). The receptor may be
CC used to raise antibodies for detection and treatment of tumours in
CC patients, and to treat e.g. pancreatic somatostatinoma, and to
CC regulate the action of somatostatin in vivo.
CC See also Q29154-7 and Q35865-6.
SQ Sequence 822 BP; 158 A; 245 C; 220 G; 194 T;

Query Match 2.1%; Score 29; DB 1; Length 822;
Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 AAGATGAAGACCGCAACCAACATCTACAT 478
|||||
Db 262 AAGATGAAGACCGCAACCAACATCTACAT 290

RESULT 11
Q75928
ID Q75928 standard; DNA; 1330 BP.
AC Q75928;
DT 17-AUG-1995 (first entry)
DE Mouse opioid receptor-like receptor MOP2 cDNA.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT Key 161..1264
FT cds /*tag= a
FT /product= mouse opioid receptor-like receptor
PN WO9428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine I, Yasuda K;
PI WPI; 95-022804/03.
DR P-PSDB; R67671.
DR Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PT Claim 28; Page 225-229; 300pp; English.
PS
```

CC The nucleotide sequence of the novel mouse opiod receptor-like receptor  
CC gene MOP2. MOP2 is a mouse receptor with pharmacological properties which  
CC are dissimilar to the properties of classic opiod receptors such kappa,  
CC delta, mu or sigma. It has been found that drug of high abuse potential  
CC or analgesic potency bind selectively to this receptor. This suggests  
CC that this receptor could be important in the development of drugs to  
CC treat addiction. Other opiod receptors isolated and produced such as the  
CC novel mouse kappa and delta opiod receptors (Q75926-7) are useful for  
CC the development of novel assays designed to select or improve substances,  
CC capable of interacting with the opiod receptor proteins, for use in  
CC diagnosis, drug design and therapeutic applications.  
SQ Sequence 1330 BP; 250 A; 368 C; 350 G; 362 T;

Query Match 1.8%; Score 25; DB 1; Length 1330;  
Best Local Similarity 100.0%; Pred. No. 0.0061;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621  
|||||  
Db 539 GACTACTACAACATGTTTACCAGCA 563

RESULT 12  
Q89233  
ID Q89233 standard; cDNA; 1567 BP.  
AC Q89233;  
DT 20-OCT-1995 (first entry)  
DE Rat opiod receptor cDNA.  
KW Opiod receptor; MOR-1; gene therapy; diagnostic; ss.  
OS Rattus sp.  
FH Key  
FT cds Location/Qualifiers  
FT 173..1276  
FT /\*tag= a

PN WO9507983-A.  
PD 23-MAR-1995.  
PF 13-SEP-1994; U10358.  
PR 13-SEP-1993; US-120601.  
PA (INDV ) UNIV INDIANA FOUND.  
PI Yu Li;  
DR WPI; 95-131351/17.  
DR P-PSDB; R71968.  
PT New nucleic acid encoding new human mu opiod receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
PS Example 9; Page 218-222; 266pp; English.  
CC The cDNA given in Q89233 was isolated from a rat brain library by  
CC low stringency hybridization with rat mu opiod receptor cDNA  
CC (Q89222). The clone encoded a 367-amino acid protein (R71968)  
CC that showed high homology with mu, kappa and delta opiod receptors  
CC but lacked affinity for their ligands, suggesting it to be  
CC a novel member of the opiod receptor family.  
SQ Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T;

Query Match 1.8%; Score 25; DB 1; Length 1567;  
Best Local Similarity 100.0%; Pred. No. 0.0061;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621  
|||||  
Db 551 GACTACTACAACATGTTTACCAGCA 575

RESULT 13  
Q90096  
ID Q90096 standard; cDNA; 2600 BP.  
AC Q90096;  
DT 03-NOV-1995 (first entry)  
DE Mouse kappa-3 opiod receptor.  
KW Kappa-3 opiod receptor; analgesia; ss.  
OS Mus sp.  
FH Key Location/Qualifiers

FT cds 299..1402  
FT /\*tag= a  
PN WO9512616-A.  
PD 11-MAY-1995.  
PF 03-NOV-1994; U12728.  
PR 05-NOV-1993; US-147949.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
PI Pan Y, Pasternak GW;  
DR WPI; 95-193814/25.  
DR P-PSDB; R74298.  
PT Nucleic acid molecule(s) encoding a kappa-3 opiod receptor, and  
PT antibody against the receptor - used to detect the receptor, and to  
PT image cell membrane-bound receptor in a subject  
PS Disclosure; Fig.1; 68pp; English.  
CC Degenerate primers based on conserved sequences of the mouse delta  
CC opiod receptor were used in PCR to amplify mouse kappa-3 opiod  
CC receptor cDNA from a mouse brain lambda ZAP cDNA library.  
SQ Sequence 2600 BP; 536 A; 680 C; 663 G; 721 T;

Query Match 1.8%; Score 25; DB 1; Length 2600;  
Best Local Similarity 100.0%; Pred. No. 0.0061;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621  
|||||  
Db 677 GACTACTACAACATGTTTACCAGCA 701

RESULT 14  
Q92972  
ID Q92972 standard; DNA; 2706 BP.  
AC Q92972;  
DT 22-DEC-1995 (first entry)  
DE Rat opiorph receptor OR7 DNA.  
KW Opiorph receptor; opiod; ss.  
OS Rattus sp.  
PN WO9519986-A1.  
PD 27-JUL-1995.  
PF 20-JAN-1995; U00939.  
PR 21-JAN-1994; US-185360.  
PA (AMCY ) AMERICAN CYANAMID CO.  
PI Eppler CM, Hultmes JD, Ozenberger BA;  
DR WPI; 95-269412/35.  
DR P-PSDB; R76638.  
PT New isolated DNA encoding an opiorph receptor - used to develop  
PT prods. for identifying opiod agonists and antagonists and for  
PT detection and manipulation  
PS Disclosure; Fig.1; 35pp; English.  
CC Primers based on rodent opoid receptors were used to amplify rat  
CC genomic DNA. Products were re-amplified and subcloned into pCR-II  
CC vector and amplified in E. coli. Plasmid DNAs were isolated, and  
CC an unspliced sequence was obtd. (Q92972) encoding the transmembrane  
CC domain opiorph receptor protein OR7.  
SQ Sequence 2706 BP; 569 A; 675 C; 704 G; 758 T;

Query Match 1.8%; Score 25; DB 1; Length 2706;  
Best Local Similarity 100.0%; Pred. No. 0.0061;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621  
|||||  
Db 485 GACTACTACAACATGTTTACCAGCA 509

RESULT 15  
T89585  
ID T89585 standard; cDNA; 1452 BP.  
AC T89585;  
DT 12-JAN-1998 (first entry)  
DE Rat orphanin FQ receptor cDNA clone LC132.  
KW Orphanin FQ receptor; binding; locomotor disease; diagnosis;

KW treatment; opioid inhibitor; opiate induced hypothermia; drug design;  
KW morphine induced analgesia; methadone specific opioid receptor; ss.

OS	Rattus sp.	Location/Qualifiers
FH	Key	1..181
FT	5'UTR	/*tag= a
FT		182..1285
FT	CDS	/*tag= b
FT		1286..1452
FT	3'UTR	/*tag= c
FT		

PN WO9707212-A1.  
PD 27-FEB-1997.  
PF 12-AUG-1996; U13305.  
PR 03-NOV-1995; US-553058.  
PR 11-AUG-1995; US-514451.  
PA (UYOR-) UNIV OREGON HEALTH SCI.  
PI Bunzow JR, Civelli O, Grandy DK, Grisel JE, Mogil JS;  
PI Monsma FJ, Nothacker H-P, Reinscheid RK;  
DR WPI; 97-165296/15.  
DR P-PSDB: W25217

P-PSDOB; W25217.  
Mammalian orphanin FQ receptor inhibitor - used in the diagnosis and treatment of locomotor disease.  
PS Claim 5; Page 42-43; 68pp; English.  
CC T89585 is rat orphanin FQ (OFQ) receptor cDNA clone LCL32. Highly specific peptides that bind the OFQ receptor were identified as  
CC OFQ receptor inhibitors. The peptides can be used to antagonise a  
CC physiological effect of an opioid in an animal. The peptides antagonise  
CC opiate induced hypothermia and morphine induced analgesia in animals.  
CC They may also be used in the diagnosis and treatment of locomotor  
CC disease. The peptides may also be used in the design of a methadone  
CC specific opioid receptor (MSOR), in drug design and for the isolation  
CC of endogenous receptors for anti-opioid agonists and antagonists found  
CC in plasma, serum, lymph, cerebrospinal fluid etc.  
SQ Sequence 1452 BP; 276 A; 414 C; 377 G; 385 T;

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Query Match      1.8%; Score 25; DB 1; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 597 GACTACTACAACAATGTTTACCAGCA 621  
 |||||  
 Db 560 GACTACTACAACAATGTTTACCAGCA 584

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Job time: 1921 sec

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OM nucleic - nucleic search, using sw model

Run on: February 17, 2000, 09:40:05 ; Search time 45.68 Seconds  
(without alignments)  
3695.460 Million cell updates/sec

Title: US-08-455-683-1  
Perfect score: 1410  
Sequence: 1 GCGCACCTTGCTGATCCCAA.....AACCAGATTACAACTGCAG 1410

Scoring table: OLIGO\_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued\_Patents\_NA:\*

Word size : 0

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5: /cgn2\_6/ptodata/2/ina/6\_COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	1.8	1452	1 US-08-149-093A-3	Sequence 3, Appli
2	25	1.8	2600	2 US-08-147-949A-1	Sequence 1, Appli
3	25	1.8	1452	2 US-08-911-245-3	Sequence 3, Appli
4	25	1.8	1452	2 US-08-553-058C-3	Sequence 3, Appli
5	25	1.8	1452	3 US-08-514-451A-3	Sequence 3, Appli
6	25	1.8	2706	3 US-08-454-549-1	Sequence 1, Appli
7	25	1.8	1567	6 PCT-US94-10358-16	Sequence 16, Appli
8	23	1.6	1829	4 US-08-411-859-1	Sequence 1, Appli
9	20	1.4	90	4 US-08-411-859-7	Sequence 7, Appli
10	20	1.4	1618	6 PCT-US94-10358-1	Sequence 1, Appli
11	20	1.4	1618	6 PCT-US94-10358-3	Sequence 3, Appli
12	20	1.4	1610	6 PCT-US94-10358-7	Sequence 7, Appli
13	17	1.2	1796	1 US-07-816-283-11	Sequence 11, Appl
14	17	1.2	2061	1 US-08-204-656B-9	Sequence 9, Appli
15	17	1.2	2061	1 US-08-470-702-5	Sequence 5, Appli
16	17	1.2	2061	1 US-08-467-831-5	Sequence 5, Appli
17	17	1.2	10564	1 US-08-206-176-5	Sequence 5, Appli
18	17	1.2	1796	2 US-08-417-103-11	Sequence 11, Appl
19	17	1.2	11725	3 US-08-756-506-1	Sequence 1, Appli
20	17	1.2	1498	4 US-08-775-428-1	Sequence 1, Appli
21	17	1.2	1324	4 US-08-330-272-1	Sequence 1, Appli
22	17	1.2	1324	6 PCT-US95-13663-1	Sequence 1, Appli
23	16	1.1	1352	1 US-07-714-819-1	Sequence 1, Appli
24	16	1.1	7350	1 US-07-865-662F-14	Sequence 14, Appl
25	16	1.1	186	1 US-08-222-177A-12	Sequence 12, Appl
26	16	1.1	1352	1 US-08-246-978A-1	Sequence 1, Appli
27	16	1.1	1731	1 US-08-203-905B-13	Sequence 13, Appl
28	16	1.1	3066	1 US-08-142-439A-1	Sequence 1, Appli
29	16	1.1	1909	1 US-08-142-439A-3	Sequence 3, Appli
30	16	1.1	3943	2 US-08-369-796-3	Sequence 3, Appli
31	16	1.1	2607	2 US-08-369-796-5	Sequence 5, Appli
32	16	1.1	5437	2 US-08-416-872-1	Sequence 1, Appli

33 16 1.1 1352 2 US-08-440-814A-1 Sequence 1, Appli  
34 16 1.1 2141 2 US-08-463-931-1 Sequence 1, Appli  
35 16 1.1 819 2 US-08-792-019B-4 Sequence 4, Appli  
36 16 1.1 2254 2 US-08-153-848-27 Sequence 27, Appl  
37 16 1.1 1500 2 US-08-443-568B-15 Sequence 15, Appl  
38 16 1.1 1711 2 US-08-749-903-2 Sequence 2, Appli  
39 16 1.1 1875 2 US-08-453-956-14 Sequence 14, Appl  
40 16 1.1 1875 2 US-08-086-631-14 Sequence 14, Appl  
41 16 1.1 885 2 US-08-411-706-3 Sequence 3, Appli  
42 16 1.1 1870 2 US-08-592-126-86 Sequence 86, Appl  
43 16 1.1 3066 3 US-08-869-477-1 Sequence 1, Appli  
44 16 1.1 1909 3 US-08-869-477-3 Sequence 3, Appli  
45 16 1.1 522 7 5391485-3 Patent No. 5391485

ALIGNMENTS

RESULT 1  
US-08-149-093A-3  
; Sequence 3, Application US/08149093A  
; Patent No. 5658783  
; GENERAL INFORMATION:  
; APPLICANT: Bunzow, James R  
; APPLICANT: Grandy, David K  
; TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific  
; TITLE OF INVENTION: Opioid Receptor Gene and Uses  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Allegretti, Ltd.  
; STREET: 10 South Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/149,093A  
; FILING DATE: 06-NOV-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5658783nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 93,311  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; TELEX: 910-221-5317  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1452 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..181  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 182..1282  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: 1283..1452  
; US-08-149-093A-3

Query Match 1.8%; Score 25; DB 1; Length 1452;  
Best Local Similarity 100.0%; Pred. No. 0.0034;

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621
    |||||
Db 560 GACTACTACAACATGTTTACCAGCA 584

RESULT 2
US-08-147-949A-1
; Sequence 1, Application US/08147949A
; Patent No. 5747279
; GENERAL INFORMATION:
; APPLICANT: Pasternak, Gavril W.
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: KAPPA3 OPIOID RECEPTORS, RECEPTORS
; TITLE OF INVENTION: ENCODED THEREBY, AND USES THEREOF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,949A
; FILING DATE: 05-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44782/JPW/JKM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2600 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 299..1401
; OTHER INFORMATION:
US-08-147-949A-1

Query Match 1.8%; Score 25; DB 2; Length 2600;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621
    |||||
Db 677 GACTACTACAACATGTTTACCAGCA 701

RESULT 3
US-08-911-245-3
; Sequence 3, Application US/08911245
; Patent No. 5821067
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R
; APPLICANT: Grandy, David K
```

```
;
; TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
; TITLE OF INVENTION: Opioid Receptor Gene and Uses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,245
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149093
; FILING DATE: 06-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5821067nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
US-08-911-245-3

Query Match 1.8%; Score 25; DB 2; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621
    |||||
Db 560 GACTACTACAACATGTTTACCAGCA 584

RESULT 4
US-08-553-058c-3
; Sequence 3, Application US/08553058C
; Patent No. 5821219
; GENERAL INFORMATION:
; APPLICANT: Grisel, Judith E.
; APPLICANT: Grandy, David K.
; APPLICANT: Mogil, Jeffrey S.
; TITLE OF INVENTION: Opioid Antagonists and Methods of Their Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston LLP
; STREET: 121 S.W. Salmon, Suite 1600
; CITY: Portland
; STATE: Oregon
```

; COUNTRY: USA
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Version WP6, ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,058C
; FILING DATE: 11/3/95
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William D. No. 5821219nan, M.D.
; REGISTRATION NUMBER: 30,878
; REFERENCE/DOCKET NUMBER: 899-40006/WDN
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
;
US-08-553-058C-3

Query Match 1.8%; Score 25; DB 2; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621
|||||
Db 560 GACTACTACAACATGTTTACCAGCA 584

RESULT 5
US-08-514-451A-3
; Sequence 3, Application US/08514451A
; Patent No. 5837809
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R.
; APPLICANT: Grandy, David K.
; APPLICANT: Civeili, Olivier
; APPLICANT: Reinscheid, Rainer K.
; APPLICANT: No. 5837809hacker, Hans-Peter
; APPLICANT: Monsma, Frederick J.
; TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID
; TITLE OF INVENTION: RECEPTOR LIGAND AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell
; ADDRESSEE: Leigh & Whinston LLP
; STREET: 121 S.W. Salmon, Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97204
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WP5.1 ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,451A
; FILING DATE: 08/11/95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/553,058
; FILING DATE: 11/13/95
; ATTORNEY/AGENT INFORMATION:
; NAME: William D. No. 5837809nan, M.D.
; REGISTRATION NUMBER: 30,878
; REFERENCE/DOCKET NUMBER: 899-45995/WDN
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
;
US-08-514-451A-3

Query Match 1.8%; Score 25; DB 3; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621
|||||
Db 560 GACTACTACAACATGTTTACCAGCA 584

RESULT 6
US-08-454-549-1
; Sequence 1, Application US/08454549
; Patent No. 5866324
; GENERAL INFORMATION:
; APPLICANT: EPPLER, C. Mark
; APPLICANT: OZENBERGER, Bradley A.
; APPLICANT: HULMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,549
; FILING DATE: 30-MAY-1995

```
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/1A818-US5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2706 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; TISSUE TYPE: Rat brain
; US-08-454-549-1

Query Match 1.8%; Score 25; DB 3; Length 2706;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621
|
Db 485 GACTACTACAACATGTTTACCAGCA 509

RESULT 7
PCT-US94-10358-16
; Sequence 16, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1567 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: 173..1273
PCT-US94-10358-16

Query Match 1.8%; Score 25; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACAACATGTTTACCAGCA 621
|
Db 551 GACTACTACAACATGTTTACCAGCA 575

RESULT 8
US-08-411-859-1
; Sequence 1, Application US/08411859
; Patent No. 5985600
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH JR., DOANE E.
; APPLICANT: EDWARDS, ROBERT H.
; TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID
; TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,859
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/929,200
; FILING DATE: 13-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: LITHGOW, TIMOTHY J.
; REGISTRATION NUMBER: 36,856
; REFERENCE/DOCKET NUMBER: 22000-20526.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1829 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29..1144
; US-08-411-859-1

Query Match 1.6%; Score 23; DB 4; Length 1829;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 591 TCCATTGACTACTACAACATGTT 613
|
Db 404 TCCATTGACTACTACAACATGTT 426
```

```
RESULT 9
US-08-411-859-7
; Sequence 7, Application US/08411859
; Patent No. 5985600
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH JR., DUANE E.
; APPLICANT: EDWARDS, ROBERT H.
; TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID
; TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,859
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/929,200
; FILING DATE: 13-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: LITHGOW, TIMOTHY J.
; REGISTRATION NUMBER: 36,856
; REFERENCE/DOCKET NUMBER: 22000-20526.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-411-859-7

Query Match 1.4%; Score 20; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 TTCTGTGATGAAACTTCAA 1198
|||||
Db 58 TTCTGTGATGAAACTTCAA 77

RESULT 10
PCT-US94-10358-1
; Sequence 1, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..1410
; PCT-US94-10358-1

Query Match 1.4%; Score 20; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 GTGGACCGCTACATGCTGT 664
|||||
Db 700 GTGGACCGCTACATGCTGT 719

RESULT 11
PCT-US94-10358-3
; Sequence 3, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
```

```

;       TELEX: 79-0924
;       INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH: 1618 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: cdna
;       FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 339..1235
;
PCT-US94-10358-3
;
Query Match          1.4%; Score 20; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 GTGACCGCTACATTGCTGT 664
      |||||||
Db 700 GTGACCGCTACATTGCTGT 719

RESULT 12
PCT-US94-10358-7
; Sequence 7, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/120.601
; APPLICATION DATE: 13 SEPTEMBER 1993
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
;
PCT-US94-10358-7
;
Query Match          1.4%; Score 20; DB 6; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 TTCTGGATGAAACTTCAA 1198
      |||||||

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Db 1256 TTCTGGATGAAACTTCAA 1275

RESULT 13
US-07-816-283-11
; Sequence 11, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816,283
; FILING DATE: 19911231
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
;
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1796 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
;
US-07-816-283-11
;
Query Match          1.2%; Score 17; DB 1; Length 1796;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 ATGAGTGTGGACCGCTA 655
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Db 565 ATGAGTGTGGACCGCTA 581

RESULT 14
US-08-204-656B-9
; Sequence 9, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuo
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.

```

```

; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,656B
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; LIBRARY: Library of chromosomal DNA from Bacillus
; LIBRARY: macerans, pMAC, generated by treating chromosomal DNA from Bacillus mac
; LIBRARY: IAM1243 with a restriction enzyme, and inserting and linking restrictio
; LIBRARY: fragments to pBR322
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2061
; OTHER INFORMATION: /note= "Nucleotides 1-2061
; OTHER INFORMATION: correspond to nucleotides 82-2142 of the Bacillus macerans
; OTHER INFORMATION: cyclomaltodextrin glucanotransferase structural gene"
US-08-204-656B-9

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Query Match      1.2%; Score 17; DB 1; Length 2061;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 130 ACGGIGACTTGGGAAGG 146
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Db 1978 ACGGTGACTTGGGAAGG 1994

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RESULT 15
US-08-470-702-5
; Sequence 5, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-470-702-5

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Query Match      1.2%; Score 17; DB 1; Length 2061;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 130 ACGGTGACTTGGGAAGG 146
|||||
Db 1978 ACGGTGACTTGGGAAGG 1994

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Search completed: February 17, 2000, 10:11:58
Job time: 1913 sec

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GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2000, 09:37:05 ; Search time 771.69 Seconds  
(without alignments)  
6898.737 Million cell updates/sec

Title: US-08-455-683-1  
Perfect score: 1410  
Sequence: 1 GCGCACCTTGCTGATCCCAA.....AACCCAGATTACAACCTGCAG 1410

Scoring table: OLIGO\_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:\*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em\_est1:\*  
2: em\_est2:\*  
3: em\_est3:\*  
4: em\_est4:\*  
5: em\_est5:\*  
6: em\_est6:\*  
7: em\_est7:\*  
8: em\_est8:\*  
9: em\_est9:\*  
10: em\_est10:\*  
11: em\_est11:\*  
12: em\_est12:\*  
13: em\_est13:\*  
14: em\_est14:\*  
15: em\_est15:\*  
16: em\_est16:\*  
17: em\_est17:\*  
18: em\_est18:\*  
19: em\_est19:\*  
20: gb\_est1:\*  
21: gb\_est2:\*  
22: gb\_est3:\*  
23: gb\_est4:\*  
24: gb\_est5:\*  
25: gb\_est6:\*  
26: gb\_est7:\*  
27: gb\_est8:\*  
28: gb\_est9:\*  
29: gb\_est10:\*  
30: gb\_est11:\*  
31: gb\_est12:\*  
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97: em\_gss10:\*  
98: em\_gss11:\*  
99: gb\_gss10:\*  
100: gb\_gss11:\*  
101: em\_gss12:\*  
102: gb\_gss12:\*  
103: gb\_gss13:\*  
104: gb\_gss14:\*  
105: gb\_gss15:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	26	1.8		153	22	R31984	R31984 yh62cl0.r1
2	22	1.6		427	64	AW047705	AW047705 UI-M-BH1-
3	20	1.4		303	37	AA683100	AA683100 ae81g12.s
4	20	1.4		401	64	AL120154	AL120154 DKF2p761A
5	20	1.4		601	74	AV387715	AV387715 AV387715
6	20	1.4		509	74	AW200827	AW200827 se9a02.y
7	20	1.4		407	82	AQ674484	AQ674484 HS_5478_B

C	8	20	1.4	555	87	AQ810283
9	19	398	41	AI009309		HS_4786_A
10	19	443	41	AI056367		EST203760
11	19	447	43	AI105468		OY48C06.X
C	12	19	1.3	890	43	AI226352
13	19	452	46	AI410541		uf07a06.Y
14	19	559	46	AI410875		EST238834
15	19	233	48	AI559367		EST239168
16	19	504	48	AI602174		tn21b12.X
C	17	19	1.3	679	50	UI-R-AB0-
18	19	302	50	AI679822		tu66b12.X
C	19	19	1.3	515	63	AV106245
20	19	616	81	AI959497		AV106245
21	19	657	82	B72980		fd10h03.Y
C	22	19	1.3	468	87	RPC111-10M2
23	19	161	103	AQ681658		HS_2161_A
C	24	19	1.3	394	103	AQ807655
C	25	19	1.3	368	105	HS_3031_B
26	19	511	105	AQ472185		CITBI-E1-
C	27	18	1.3	352	21	AQ472191
28	18	433	23	AQ642479		E1-
C	29	18	1.3	384	25	AQ661946
30	18	414	25	R04688		HS_2093_B
C	31	18	1.3	448	25	R04688
32	18	429	25	H41020		pk27e08.r1
33	18	349	27	N57941		yp72dl1.s1
34	18	374	28	N57941		yv61g04.s1
35	18	523	28	N62652		zal4d10.s1
36	18	651	29	N78731		zb05a11.s1
37	18	680	29	W09072		ma62f06.r1
C	38	18	1.3	466	30	AA000300
39	18	206	31	AA130056		mg32a09.r
40	18	364	32	AA196290		Cl15712
41	18	477	33	AA218901		Cl15712
42	18	521	33	AA317847		Cl15915
C	43	18	1.3	469	34	AA130056
C	44	18	1.3	580	35	AA196290
C	45	18	1.3	383	36	AA218901

AQ810283	HS_4786_A
AI009309	EST203760
AI056367	OY48C06.X
AI105468	EST214757
AI226352	uf07a06.Y
AI410541	EST238834
AI410875	EST239168
AI559367	tn21b12.X
AI602174	UI-R-AB0-
AI679822	tu66b12.X
AV106245	AV106245
AI959497	fd10h03.Y
B72980	RPC111-10M2
AQ681658	HS_2161_A
AQ807655	HS_3031_B
AQ472185	CITBI-E1-
AQ472191	E1-
AQ642479	RPC193-EC
AQ661946	HS_2093_B
R04688	pk27e08.r1
H41020	yp72dl1.s1
N57941	yv61g04.s1
N62652	zal4d10.s1
N78731	zb05a11.s1
W09072	ma62f06.r1
AA000300	mg32a09.r
Cl15712	Cl15712
Cl15915	Cl15915
AA130056	zn62e11.r
AA196290	zp92g04.s
AA218901	zq15e05.S
AA317847	EST19840
AA366615	EST77582
AA407460	EST00811
AA447244	zw93c04.r
AA468769	ne09f02.s
AA565655	nk26g06.s
AA610438	np91d02.s

ALIGNMENTS

RESULT	1
R31984	
LOCUS	R31984 153 bp mRNA EST 28-APR-1995
DEFINITION	yh62c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134322 5' similar to gb:L25119 MU-TYPE OPIOID RECEPTOR (HUMAN); mRNA sequence.
ACCESSION	R31984
VERSION	R31984.1 GI:787827
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 153)
TITLE	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
JOURNAL	The WashU-Merck EST Project
COMMENT	Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 947 High quality sequence stops: 120 Source: IMAGE Consortium, LLNL

FEATURES	Location/Qualifiers	High quality sequence stop: 120.
source	1..153	
	/organism="Homo sapiens"	
	/db_xref="GDB:540134"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:134322"	
	/clone_lib="Soares placenta Nb2HP"	
	/sex="Female"	
	/dev_stage="placenta obtained at birth (full term)"	
	/lab_host="DH10B (ampicillin resistant)"	
	/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAGAATTCGGCGCCGAGGAATTTT TTTT TTTT TTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "	
BASE COUNT	25 a 49 c 37 g 42 t	
ORIGIN		
	Query Match 1.8%; Score 26; DB 22; Length 153;	
	Best Local Similarity 100.0%; Pred. No. 0.0035;	
	Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	915 GTCTGCTACACCCCTGATGATCCTGCG 940	
Db	45 GTCTGCTACACCCCTGATGATCCTGCG 70	
RESULT	2	
AW047705/c		
LOCUS	AW047705 427 bp mRNA EST 18-SEP-1999	
DEFINITION	UI-M-BH1-alo-f-04-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alo-f-04-0-UI 3', mRNA sequence.	
ACCESSION	AW047705	
VERSION	AW047705.1 GI:5908234	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 427)	
TITLE	Bonaldo,M.F., Lennon,G. and Soares,M.B.	
JOURNAL	Normalization and subtraction: two approaches to facilitate gene discovery	
MEDLINE	Genome Res. 6 (9), 791-806 (1996)	
COMMENT	97044477 On Jun 22, 1998 this sequence version replaced gi:3246886. Contact: Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 9890 Email: mEST@mail.nih.gov The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized cerebellum library cDNA Library Preparation: M.B. Soares lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.	

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Seq primer: M13 Forward
POLYA=Yes.
FEATURES
    source
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                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UI-M-BH1-alo-f-04-0-UI"
                /clone_lib="NIH_BMAP_M_S2"
                /dev_stage="27-32 days"
                /lab_host="DH10B (Life Technologies)"
                /note="Vector: pT713D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; The
                NIH_BMAP_M_S2 library is a subtracted library derived from
                NIH_BMAP_M_S1, which in turn is a subtracted library
                derived from a mixture of normalized libraries from ten
                regions of the mouse brain (cerebellum, brain stems,
                olfactory bulbs, hypothalamus, cortex, amygdala, basal
                ganglia, pineal gland, striatum, hippocampus). The driver
                used for subtraction consisted of a pool of 5,000 clones
                from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
                obtained from non-normalized and normalized mouse brain
                spinal cord libraries.
                TAG_LIB=NIH_BMAP_M_S2
                TAG_TISSUE=cerebellum
                TAG_SEQ=GACTC"
BASE COUNT      119 a      104 c      107 g      97 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 22; DB 64; Length 427;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 TACTACACATGTTTACCAGCA 621
      |||||
Db 355 TACTACACATGTTTACCAGCA 334

RESULT 3
LOCUS      AA683100      303 bp      mRNA      EST      15-DEC-1997
DEFINITION      ae81g12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone
IMAGE:970630 3' similar to SW:MAPA_RAT P34926
MICROTUBULE-ASSOCIATED PROTEIN 1A ; mRNA sequence.
ACCESSION      AA683100
VERSION      AA683100.1 GI:2668991
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 303)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,I., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
On Sep 19, 1997 this sequence version replaced gi:1520424.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 229.
Location/Qualifiers
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                /db_xref="taxon:10090"
                /clone="UI-M-BH1-alo-f-04-0-UI"
                /clone_lib="NIH_BMAP_M_S2"
                /dev_stage="27-32 days"
                /lab_host="DH10B (Life Technologies)"
                /note="Vector: pT713D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; The
                NIH_BMAP_M_S2 library is a subtracted library derived from
                NIH_BMAP_M_S1, which in turn is a subtracted library
                derived from a mixture of normalized libraries from ten
                regions of the mouse brain (cerebellum, brain stems,
                olfactory bulbs, hypothalamus, cortex, amygdala, basal
                ganglia, pineal gland, striatum, hippocampus). The driver
                used for subtraction consisted of a pool of 5,000 clones
                from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
                obtained from non-normalized and normalized mouse brain
                spinal cord libraries.
                TAG_LIB=NIH_BMAP_M_S2
                TAG_TISSUE=cerebellum
                TAG_SEQ=GACTC"
BASE COUNT      119 a      104 c      107 g      97 t
ORIGIN

Seq primer: M13 Forward
POLYA=Yes.
FEATURES
    source
        Location/Qualifiers
            1..427
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UI-M-BH1-alo-f-04-0-UI"
                /clone_lib="NIH_BMAP_M_S2"
                /dev_stage="27-32 days"
                /lab_host="DH10B (Life Technologies)"
                /note="Vector: pT713D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; The
                NIH_BMAP_M_S2 library is a subtracted library derived from
                NIH_BMAP_M_S1, which in turn is a subtracted library
                derived from a mixture of normalized libraries from ten
                regions of the mouse brain (cerebellum, brain stems,
                olfactory bulbs, hypothalamus, cortex, amygdala, basal
                ganglia, pineal gland, striatum, hippocampus). The driver
                used for subtraction consisted of a pool of 5,000 clones
                from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
                obtained from non-normalized and normalized mouse brain
                spinal cord libraries.
                TAG_LIB=NIH_BMAP_M_S2
                TAG_TISSUE=cerebellum
                TAG_SEQ=GACTC"
BASE COUNT      119 a      104 c      107 g      97 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 22; DB 64; Length 427;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 TACTACACATGTTTACCAGCA 621
      |||||
Db 355 TACTACACATGTTTACCAGCA 334

RESULT 3
LOCUS      AA683100      303 bp      mRNA      EST      15-DEC-1997
DEFINITION      ae81g12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone
IMAGE:970630 3' similar to SW:MAPA_RAT P34926
MICROTUBULE-ASSOCIATED PROTEIN 1A ; mRNA sequence.
ACCESSION      AA683100
VERSION      AA683100.1 GI:2668991
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 303)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,I., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
On Sep 19, 1997 this sequence version replaced gi:1520424.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 229.
Location/Qualifiers
FEATURES
    source
        Location/Qualifiers
            1..427
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UI-M-BH1-alo-f-04-0-UI"
                /clone_lib="NIH_BMAP_M_S2"
                /dev_stage="27-32 days"
                /lab_host="DH10B (Life Technologies)"
                /note="Vector: pT713D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; The
                NIH_BMAP_M_S2 library is a subtracted library derived from
                NIH_BMAP_M_S1, which in turn is a subtracted library
                derived from a mixture of normalized libraries from ten
                regions of the mouse brain (cerebellum, brain stems,
                olfactory bulbs, hypothalamus, cortex, amygdala, basal
                ganglia, pineal gland, striatum, hippocampus). The driver
                used for subtraction consisted of a pool of 5,000 clones
                from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
                obtained from non-normalized and normalized mouse brain
                spinal cord libraries.
                TAG_LIB=NIH_BMAP_M_S2
                TAG_TISSUE=cerebellum
                TAG_SEQ=GACTC"
BASE COUNT      119 a      104 c      107 g      97 t
ORIGIN
```

```
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
    source
        Location/Qualifiers
            1..303
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:970630"
                /clone_lib="Stratagene schizo brain S11"
                /sex="male"
                /tissue_type="schizophrenic brain S-11 frontal lobe"
                /dev_stage="34 years old"
                /lab_host="SOLR (kanamycin resistant)"
                /note="Vector: Bluescript SK-; Site_1: EcoRI; Library
                constructed from S-11 frontal lobe, male, 34 years old,
                50% caucasian, 50% Aleutian. Schizophrenic suicide.
                Random primed into EcoRI site of ZAP II Vector. Mass
                excised. Custom library. Avg insert length 1.4kb.
                Material obtained by Johnston N., Torrey, E.F., Yolken R.,
                and the Stanley Neuropathology Consortium - Analysis of
                RNAs from the Brains of Individuals with Psychiatric
                Diseases (Unpublished) Stanley Neurovirology Laboratory,
                Johns Hopkins School of Medicine, Baltimore MD."
BASE COUNT      51 a      118 c      68 g      56 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 37; Length 303;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 CACAGCTGCCCTCTCCAGCT 1119
      |||||
Db 113 CACAGCTGCCCTCTCCAGCT 132

RESULT 4
LOCUS      AL120154      401 bp      mRNA      EST      27-SEP-1999
DEFINITION      DKFZp761A137_r1 761 (synonym: hany2) Homo sapiens cDNA clone
IMAGE:970630 5' mRNA sequence.
ACCESSION      AL120154
VERSION      AL120154.1 GI:5926053
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 401)
AUTHORS      Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehrer, et al.)
Unpublished (1999)
On Feb 18, 1999 this sequence version replaced gi:4297623.
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFz within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
FEATURES
    source
        Location/Qualifiers
            1..401
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="DKFZp761A137"
                /clone_lib="761 (synonym: hany2)"
                /tissue_type="amygdala"
                /dev_stage="adult"
                /lab_host="DH10B"
                /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      64 a      157 c      93 g      86 t
ORIGIN
```

Query Match 1.4%; Score 20; DB 64; Length 401;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 CACAGCTGCCCTCTCCAGCT 1119  
|||||  
Db 61 CACAGCTGCCCTCTCCAGCT 80

RESULT 5  
AV3877715  
LOCUS AV3877715 601 bp mRNA EST 09-DEC-1999  
DEFINITION AV3877715 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii  
cDNA clone CM028ell\_r, mRNA sequence.  
ACCESSION AV3877715  
VERSION AV3877715.1 GI:6541931  
KEYWORDS EST.  
SOURCE Chlamydomonas reinhardtii.  
ORGANISM Chlamydomonas reinhardtii  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 601)  
AUTHORS Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.  
TITLE A Large Scale Structural Analysis of cDNAs in a Unicellular Green  
Alga, Chlamydomonas reinhardtii. I. Generation of 3451  
non-redundant Expressed Sequence Tags  
JOURNAL DNA Res. (1999) In press  
COMMENT On Jul 8, 1999 this sequence version replaced gi:5422471.  
Contact: yasukazu Nakamura  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.  
Location/Qualifiers

FEATURES  
source  
1..601  
/organism="Chlamydomonas reinhardtii"  
/strain="C9"  
/db\_xref="taxon:3055"  
/clone="CM028ell\_r"  
/clone\_lib="Chlamydomonas reinhardtii C9"  
/dev\_stage="photoautotrophic growth"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 138 a 171 c 165 g 127 t  
ORIGIN  
Query Match 1.4%; Score 20; DB 74; Length 601;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 CAACATCTACATATTTAACC 486  
|||||  
Db 118 CAACATCTACATATTTAACC 137

RESULT 6  
AW200827/c  
LOCUS AW200827 509 bp mRNA EST 30-NOV-1999  
DEFINITION se94a02.y1 Gm-cl027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
Gm-cl027-387 5' similar to TR:Q9ZUS7 Q9ZUS7 F3G5.18 PROTEIN. ;,  
mRNA sequence.  
ACCESSION AW200827  
VERSION AW200827.1 GI:6481556  
KEYWORDS EST.  
SOURCE soybean.  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core  
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Glycine.

REFERENCE 1 (bases 1 to 509)  
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,  
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,C.,  
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,  
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,  
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.  
TITLE Public Soybean EST Project  
JOURNAL Unpublished (1999)  
COMMENT On Feb 18, 1999 this sequence version replaced gi:4299224.  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: Genome Systems, Inc. 4633 World  
Parkway Circle St. Louis, Missouri 63134 For further information  
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)  
427-3324 or contact: clones@genomesystems.com or  
info@genomesystems.com web site: www.genomesystems.com  
High quality sequence stop: 406.

FEATURES  
source  
Location/Qualifiers  
1..509  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl027-387"  
/clone\_lib="Gm-cl027"  
/tissue\_type="cotyledons of 3- and 7-day-old Williams  
seedlings"  
/lab\_host="DH10B"  
/note="Vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2:  
XhoI; This cDNA library was constructed from mRNA isolated  
from cotyledons of 3- and 7-day-old Williams seedlings  
which were propagated on paper towels with distilled  
water. The cotyledons were flash-frozen in liquid  
nitrogen, then lyophilized for 72 hours. Unequal amounts  
of mRNA was used for cDNA synthesis. Stratagene's cDNA  
Synthesis Kit (catalog number 200401) was used to  
synthesize the cDNA. First- stranded synthesis was  
performed with 5-methyl dCTP, hence the ligated cDNA was  
hemimethylated. A modification of Stratagene's  
first-strand synthesis primer was used. An anchor  
nucleotide (V=A, C, or G) was added to the 3' end of the  
primer [GAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)18] to anchor  
the primer at the 5' end of the poly(A) tract. After  
second- strand synthesis, the cDNA ends were filled in  
with cloned Pfu DNA, ligated to EcoRI adapters and  
subsequently phosphorylated. The XhoI site within the  
first-strand synthesis primer was then restricted by  
digestion with XhoI; all XhoI sites in the cDNA would be  
protected by their hemimethylated status. The cDNA  
constructs were size-fractionated with a 500 bp cutoff,  
using GibcoBRL Life Technologies' cDNA Size Fractionation  
column. The column eluent was then ligated into  
Stratagene's pBluescript(tm) II XR Predigested vector  
(pBluescript II SK(+)) that has been digested with EcoRI  
and XhoI, and phosphorylated by Stratagene). 97% of the  
white and blue colonies appear to contain recombinant  
plasmids with cDNA inserts, based on size (n=30). This  
library was constructed by Dr. Paul Keim and Dr. Virginia  
Coryell."

BASE COUNT 139 a 138 c 96 g 135 t 1 others  
ORIGIN  
Query Match 1.4%; Score 20; DB 74; Length 509;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 551 TTCTTGGCCTTTTGGAGATG 570  
|||||

```
Db 229 TTCITGGCCCTTTTGGAGATG 210

RESULT 7
AQ674484/c
LOCUS      407 bp      DNA      24-JUN-1999
DEFINITION HS_5478_B2_G10_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=1054 Col=20 Row=N, genomic survey sequence.
ACCESSION  AQ674484
VERSION     AQ674484.1 GI:5207230
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 407)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL    Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE    99380589
COMMENT    Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 1054 row: N column: 20
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 407.
            Location/Qualifiers
                1..407
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="Plate=1054 Col=20 Row=N"
                /clone_lib="RPCI-11 Human Male BAC Library"
                /sex="male"
                /note="Vector: pBACe3.6; Genomic sequence of BAC ends"

BASE COUNT  145 a 104 c 73 g 85 t
ORIGIN

Query Match      1.4%; Score 20; DB 82; Length 407;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 377 TGTCTACTCTGTGGTATTG 396
      |||||
Db 271 TGTCTACTCTGTGGTATTG 252

RESULT 8
AQ810283/c
LOCUS      555 bp      DNA      10-AUG-1999
DEFINITION HS_4786_A1_E12_T7A CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=4786 Col=23 Row=I, genomic survey
            sequence.
ACCESSION  AQ810283
VERSION     AQ810283.1 GI:5729525
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
```

```
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 555)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL    Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE    99380589
COMMENT    On Feb 19, 1999 this sequence version replaced gi:4143382.
            Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 4786 row: I column: 23
            Seq primer: I7
            Class: BAC ends
            High quality sequence stop: 555.
            Location/Qualifiers
                1..555
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="Plate=4786 Col=23 Row=I"
                /clone_lib="CIT Approved Human Genomic Sperm Library D"
                /sex="male"
                /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
                E-Coli DH10B"

BASE COUNT  190 a 137 c 98 g 128 t 2 others
ORIGIN

Query Match      1.4%; Score 20; DB 87; Length 555;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 377 TGTCTACTCTGTGGTATTG 396
      |||||
Db 286 TGTCTACTCTGTGGTATTG 267

RESULT 9
AI009309
LOCUS      398 bp      mRNA      25-JAN-1999
DEFINITION EST203760 Normalized rat heart, Bento Soares Rattus sp. cDNA clone
            RHEBD13 3' end, mRNA sequence.
ACCESSION  AI009309
VERSION     AI009309.1 GI:3223141
KEYWORDS   EST.
SOURCE     Rattus sp.
ORGANISM   Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE  1 (bases 1 to 398)
AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
            Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
            Unpublished (1998)
            On Jan 17, 1998 this sequence version replaced gi:2045441.
            Contact: Lee, NH
            ATCC
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            Seq primer: M13-21.
            Location/Qualifiers
```

```
source
1. .398
/organism="Rattus sp."
/db_xref="ATCC (inhost):2020351"
/db_xref="taxon:10118"
/clone="RHEBD13"
/clone_lib="Normalized rat heart, Bento Soares"
/note="Organ: heart; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 102 a 82 c 94 g 120 t
ORIGIN

Query Match 1.3%; Score 19; DB 41; Length 398;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 CTCTGGTCATGTTTGTCAT 436
|||||
Db 321 CTCTGGTCATGTTTGTCAT 339

RESULT 10
AI056367 443 bp mRNA EST 24-SEP-1998
LOCUS
DEFINITION oy48c06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1669066 3',
mRNA sequence.
ACCESSION AI056367
VERSION AI056367.1 GI:3330233
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 443)
AUTHORS NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1404573.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 593 Std Error: 0.00
Seq primer: -40ml3 fwd. BT from Amersham.
Location/Qualifiers
1. .443
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1669066"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCCGCATATCTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 85 a 106 c 119 g 132 t
```

```
ORIGIN

Query Match 1.3%; Score 19; DB 41; Length 443;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 777 GGCACCAAGTCAGGGAAG 795
|||||
Db 152 GGCACCAAGTCAGGGAAG 170

RESULT 11
AI105468 447 bp mRNA EST 20-JAN-1999
LOCUS
DEFINITION EST214757 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
RK1BK82 3' end, mRNA sequence.
ACCESSION AI105468
VERSION AI105468.1 GI:3709542
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
REFERENCE 1 (bases 1 to 447)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: TC53042
Contact: Lee, NH
ATCC
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
Location/Qualifiers
1. .447
/organism="Rattus sp."
/db_xref="ATCC (inhost):2025917"
/db_xref="taxon:10118"
/clone="RK1BK82"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 122 a 85 c 99 g 141 t
ORIGIN

Query Match 1.3%; Score 19; DB 43; Length 447;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 CTCTGGTCATGTTTGTCAT 436
|||||
Db 424 CTCTGGTCATGTTTGTCAT 442

RESULT 12
AI226352/c 890 bp mRNA EST 29-OCT-1998
LOCUS
DEFINITION uf07a06.y1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
IMAGE:1510642 5' similar to SW:ARG2_MOUSE 008691 ARGINASE II
PRECURSOR ;, mRNA sequence.
ACCESSION AI226352
VERSION AI226352.1 GI:3809405
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
```

REFERENCE  
AUTHORS  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 890)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.  
TITLE  
The WashU-HHMI Mouse EST Project  
JOURNAL  
Unpublished (1996)  
COMMENT  
On Jan 19, 1998 this sequence version replaced gi:2286647.  
Contact: Marra M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:937494  
Seq primer: -40RP from Gibco  
High quality sequence stop: 405.

FEATURES  
source  
1. .890  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1510642"  
/clone\_lib="Soares mouse mammary gland NMLMG"  
/sex="female (lactating)"  
/tissue\_type="mammary gland"  
/lab\_host="DH10B"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from mammary  
gland tissue from a lactating female, and was then primed  
with a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified pT7T3 vector. Library is normalized. Library  
was constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 223 a 230 c 217 g 219 t 1 others  
ORIGIN

Query Match 1.3%; Score 19; DB 43; Length 890;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 853 ATCTCTTCATGAAGATCTG 871  
Db 671 ATCTCTTCATGAAGATCTG 653  
RESULT 13  
AI410541  
LOCUS  
AI410541 452 bp mRNA EST 09-FEB-1999  
DEFINITION  
EST238834 Normalized rat heart, Bento Soares Rattus sp. cDNA clone  
RHECY03 3' end, mRNA sequence.  
ACCESSION  
AI410541 GI:4254045  
VERSION  
AI410541.1  
KEYWORDS  
EST.  
SOURCE  
Rattus sp.  
ORGANISM  
Rattus sp.

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
1 (bases 1 to 452)  
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,  
Kerlavage,A.R. and Adams,M.D.  
TITLE  
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat  
Gene Index  
JOURNAL  
Unpublished (1998)  
COMMENT  
On Apr 7, 1998 this sequence version replaced gi:3034510.  
Contact: Lee, NH  
ATCC

The Institute for Genomic Research  
9712, Medical Center Drive, Rockville, MD 20850, USA  
Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: nhlee@tigr.org  
Seq primer: M13-21.  
FEATURES  
Location/Qualifiers  
1. .452  
/organism="Rattus sp."  
/db\_xref="taxon:10118"  
/clone="RHECY03"  
/clone\_lib="Normalized rat heart, Bento Soares"  
/note="Organ: heart; Vector: pT7T3Pac; Site\_1: EcoRI;  
Site\_2: NotI"  
BASE COUNT 119 a 86 c 97 g 150 t  
ORIGIN

Query Match 1.3%; Score 19; DB 46; Length 452;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 CTCGTGTCATGTTGTCAI 436  
Db 424 CTCGTGTCATGTTGTCAI 442  
RESULT 14  
AI410875  
LOCUS  
AI410875 559 bp mRNA EST 09-FEB-1999  
DEFINITION  
EST239168 Normalized rat heart, Bento Soares Rattus sp. cDNA clone  
RHECY48 3' end, mRNA sequence.  
ACCESSION  
AI410875  
VERSION  
AI410875.1 GI:4254379  
KEYWORDS  
EST.  
SOURCE  
Rattus sp.  
ORGANISM  
Rattus sp.

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
1 (bases 1 to 559)  
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,  
Kerlavage,A.R. and Adams,M.D.  
TITLE  
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat  
Gene Index  
JOURNAL  
Unpublished (1998)  
COMMENT  
On Apr 7, 1998 this sequence version replaced gi:3034844.  
Contact: Lee, NH  
ATCC

The Institute for Genomic Research  
9712, Medical Center Drive, Rockville, MD 20850, USA  
Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: nhlee@tigr.org  
Seq primer: M13-21.  
FEATURES  
Location/Qualifiers  
1. .559  
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/db\_xref="taxon:10118"  
/clone="RHECY48"  
/clone\_lib="Normalized rat heart, Bento Soares"  
/note="Organ: heart; Vector: pT7T3Pac; Site\_1: EcoRI;  
Site\_2: NotI"

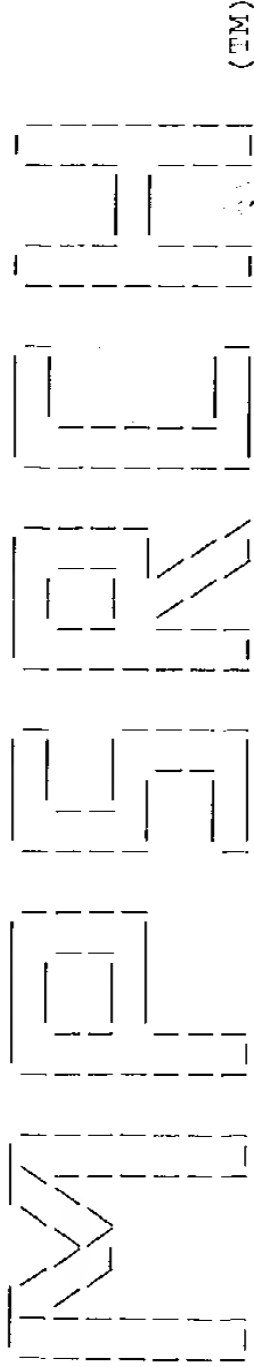
BASE COUNT 153 a 107 c 128 g 171 t  
ORIGIN

Query Match 1.3%; Score 19; DB 46; Length 559;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 CTCGTGTCATGTTGTCAI 436  
Db 424 CTCGTGTCATGTTGTCAI 442

RESULT 15  
AI559367 233 bp mRNA EST 12-MAY-1999  
LOCUS tn21b12.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2168255 3',  
DEFINITION mRNA sequence.  
ACCESSION AI559367  
VERSION AI559367.1 GI:4509572  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 233)  
AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGAP), Tumor Gene Index  
JOURNAL Unpublished (1998)  
COMMENT On Jun 5, 1998 this sequence version replaced gi:3189024.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 568 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 224  
POLYA=No.  
FEATURES Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2168255"  
/clone\_lib="NCI\_CGAP\_Brn25"  
/tissue\_type="anaplastic oligodendroglioma"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dt) primer [5'  
TGTTACCAATCTGAAGTGGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
Library is normalized, and was constructed by Bento  
Soares and M.Fatima Bonaldo."  
BASE COUNT 53 a 46 c 53 g 81 t  
ORIGIN  
Query Match 1.3%; Score 19; DB 48; Length 233;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 777 GGCACCAAGTCAGGGAAG 795  
|||||  
Db 128 GGCACCAAGTCAGGGAAG 146

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(TM)

\*\*\*\*\*

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 17 11:11:36 2000; MasPar time 23.72 Seconds  
Tabular output not generated. 340.625 Million cell updates/sec

Title: >US-08-455-683-2  
Description: (1-380) from US08455683.pep  
Perfect Score: 2839  
Sequence: 1 MESPIQIFRGDPGPTCPSA.....RNTVQDPASMRDVGGMKPV 380  
Scoring table: PAM 150  
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq35  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39

Statistics: Mean 35.005; Variance 158.855; scale 0.220

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	2839	100.0	380	13	Mouse kappa opioid re	7.33e-252
2	2839	100.0	380	34	Mouse kappa opiate re	7.33e-252
3	2829	99.6	380	14	Rat kappa opiate rece	6.49e-251
4	2823	99.4	380	14	Mammalian kappa opioi	2.40e-250
5	2746	96.7	380	27	Human kappa opioid re	4.66e-243
6	2746	96.7	380	17	Human kappa opioid re	4.66e-243
7	2737	96.4	427	27	Human kappa opioid re	3.31e-242
8	2559	90.1	424	27	Human kappa opioid re	2.29e-225
9	2130	75.0	295	12	Human kappa opioid re	7.59e-185
10	1683	59.3	356	11	Murine mu-subtype opi	9.39e-143
11	1678	59.1	398	34	Mouse mu opiate recep	2.77e-142
12	1677	59.1	400	13	Human mu opiate recep	3.44e-142
13	1676	59.0	398	14	Rat mu opiate recepto	4.27e-142
14	1674	59.0	398	13	Rat mu opiate recepto	6.58e-142
15	1675	59.0	400	14	Human mu opiate recep	5.30e-142
16	1610	56.7	372	14	Rat delta opiate rece	6.76e-136

17	1597	56.3	372	9	R48629	Sequence of murine de	1.12e-134
18	1597	56.3	372	13	R67670	Mouse delta opioid re	1.12e-134
19	1597	56.3	372	34	W44938	Mouse delta opiate re	1.12e-134
20	1499	52.8	371	10	R66503	Murine delta opioid r	1.76e-125
21	1473	51.9	367	13	R71968	Rat opioid receptor.	4.81e-123
22	1471	51.8	367	13	R67671	Mouse opioid receptor	7.40e-123
23	1464	51.6	367	14	R76638	Rat opiorph receptor	3.35e-122
24	1444	50.9	367	25	W26582	Rat methadone-specifi	2.51e-120
25	1444	50.9	367	36	W80549	Rat methadone-specifi	2.51e-120
26	1444	50.9	367	24	W25217	Rat orphanin FQ recep	2.51e-120
27	1195	42.1	367	13	R74298	Mouse kappa-3 opioid	4.77e-97
28	980	34.5	391	7	R39260	Murine somatostatin r	4.77e-77
29	976	34.4	391	7	R39259	Human somatostatin re	1.12e-76
30	922	32.5	369	7	R39262	Murine somatostatin r	1.13e-71
31	912	32.1	369	7	R39261	Human somatostatin re	9.49e-71
32	912	32.1	369	19	R97269	Human somatostatin re	9.49e-71
33	901	31.7	369	5	R27504	Pituitary somatostati	9.88e-70
34	850	29.9	333	13	R72985	Epsilon opioid recept	5.09e-65
35	817	28.8	322	16	R48754	Rat RGH G-protein cou	5.62e-62
36	817	28.8	322	19	W02726	Rat RGHjp G-protein c	5.62e-62
37	815	28.7	418	7	R39263	Human somatostatin re	8.59e-62
38	792	27.9	328	13	R72984	Epsilon opioid recept	1.13e-59
39	732	25.8	428	7	R39264	Murine somatostatin r	3.68e-54
40	679	23.9	242	23	W10017	G-protein coupled rec	2.63e-49
41	623	21.9	355	25	W26588	Human MIP-1 alpha/RAN	3.39e-44
42	623	21.9	355	11	R52749	C-C chemokine recepto	3.39e-44
43	623	21.9	355	24	W25751	Human MIP-1alpha/RANT	3.39e-44
44	616	21.7	372	30	W52251	Rat galanin receptor	1.47e-43
45	615	21.7	372	29	W40136	Rat GalR2 receptor pr	1.81e-43

ALIGNMENTS

RESULT 1  
ID R67669 standard; Protein; 380 AA.  
AC R67669;  
DT 17-AUG-1995 (first entry)  
DE Mouse kappa opioid receptor MORK1.  
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;  
KW transmembrane domain; somatostatin; receptor; human; expression vector;  
KW truncate; chimaeric; assay; probe.  
OS Mus musculus.  
PN W09428132-A.  
PD 08-DEC-1994.  
PF 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.  
PR 30-JUL-1993; US-100694.  
PR 05-NOV-1993; US-147592.  
PA (ARCH-) ARCH DEV CORP.  
PI Bell GI, Reisine T, Yasuda K;  
DR WPI: 95-022804/03.  
DR N-PSDB; Q75926.  
PT Polynucleotides and peptides derived from opioid receptor  
PT polypeptides - for use in therapeutic compositions and in  
PT screening assays for useful drug substances.  
PS Claim 8; Page 207-211; 300pp; English.  
CC The amino acid sequence of the novel mouse kappa opioid receptor MORK1.  
CC The corresponding gene was isolated from a mouse brain cDNA library using  
CC a fragment (amplified from the cDNA library with primers Q75929-30) as a  
CC probe. The primers are based on the conserved sequences present in the  
CC second and third transmembrane domains of somatostatin (SRIF) receptor  
CC subtypes SST1, SST2 and SST3. The 1.2 kb PstI fragment from the mouse  
CC kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV  
CC promoter-based expression vector pCMV-6b. The resultant construct  
CC pCMV-msl-1 was transfected into COS-1 cells for protein production. The  
CC gene encoding the opioid receptor can be used to produce complete,  
CC truncated or chimaeric opioid receptor proteins. The opioid receptors  
CC thus produced are useful for the development of novel assays designed to  
CC select or improve substances, capable of interacting with the opioid  
CC receptor proteins, for use in diagnosis, drug design and therapeutic  
CC applications.  
SQ Sequence 380 AA;

Query Match 100.0%; Score 2839; DB 13; Length 380;  
Best Local Similarity 100.0%; Pred. No. 7.33e-252;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mespiqifrgdpgptcpsacllpnssswfnwaesdsgsvgsdqqlsahispaipv 60  
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QY 1 MESPIQIFRGDPGPTCPSACLLPNSSSWFNPWAESDSNGSVGSEDQQLSAHISPAIPV 60  
|||||

Db 61 iitavysvfvvlgvgnslvmfviirytkmktatniyifnlaladalvtttmpfqsavyl 120  
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QY 61 IITAVYSVVFVVGVLGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQSAVYL 120  
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Db 121 mnswpfgdvclckivisidyynmftsifltmmsvdryiavchp vkaldfrt plkakiini 180  
|||||  
QY 121 MNSWPFQDVLCCKIVISIDYNNMFTSIFLTMMMSVDRYIAVCHP VKALDFRTPLKAKIINI 180  
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Db 181 ciwllassvgisaivlggtkvredvdiacsqfpddesyswldf mki cvfvfafvipvl 240  
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QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWDLFMKICVVFVFAVIPVL 240  
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Db 241 iivvcytlmilrlksvrlsgsrekdnrlrritklvlvvvavfiicwt pihifilvealg 300  
|||||  
QY 241 IIVVCYTLMLRLKSVRLSGSREKDRNLRRITKLVVVVAVFIICWTP IHI FILVEALG 300  
|||||

Db 301 stshstaalssyffcialgytnsslnp vlyafldenfkrcfrdfc fipk mmerqstnrv 360  
|||||  
QY 301 STSHSTAALSSYFFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360  
|||||

Db 361 rntvgdpasmrdvvgmnkp v 380  
|||||  
QY 361 RNTVQDPASMRDVGGMNKP V 380  
|||||

RESULT 2  
ID W44939 standard; Protein; 380 AA.  
AC W44939;  
DI 28-OCT-1998 (first entry)  
DE Mouse kappa opiate receptor.  
KW Mouse; kappa opiate receptor; transgenic animal; mammal; identification;  
KW exon; nervous tissue; pain; drug addiction; transplant rejection;  
KW immunosuppressant; analgesic; morphine; side effect.  
OS Mus sp.  
PN WO9802534-A2.  
PD 22-JAN-1998.  
PF 11-JUL-1997; FO1282.  
PR 15-JUL-1996; FR-008810.  
PA (CNRS ) CENT NAT RECH SCI.  
PI Dierich A, Kieffer BL, LeMeur M, Matthes HWD, Simonin FH;  
DR WPI; 98-110582/10.  
DR N-PSDB; V49254.  
PT Transgenic animals defective in one type of opioid receptor - used  
PT to identify agents for treatment of pain, drug addiction and  
PI transplant rejection, lacking side effects of known opiate(s)  
PS Disclosure; Fig 13; 58pp; French.  
CC This sequence represents the mouse kappa opiate receptor. The gene  
CC sequence is used to generate a transgenic non-human mammal for  
CC identifying agents for treating disorders associated with opiate  
CC receptors. In the mammal, the expression of the gene encoding the  
CC opiate receptor is modified, particularly by the deletion of an exon  
CC and/or insertion of a marker gene, e.g. the neomycin resistance gene,  
CC into the sequence. Especially the expression of the gene is altered  
CC in nervous tissue. The agents are potentially useful for treating  
CC severe pain (chronic or acute), drug addiction and/or prevention or  
CC treatment of transplant rejection (as immunosuppressants). The method  
CC may isolate and identify powerful analgesics that lack morphine-like  
CC side effects.  
SQ Sequence 380 AA;

Query Match 100.0%; Score 2839; DB 34; Length 380;  
Best Local Similarity 100.0%; Pred. No. 7.33e-252;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mespiqifrgdpgptcpsacllpnssswfnwaesdsgsvgsdqqlsahispaipv 60  
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QY 1 MESPIQIFRGDPGPTCPSACLLPNSSSWFNPWAESDSNGSVGSEDQQLSAHISPAIPV 60  
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Db 61 iitavysvfvvlgvgnslvmfviirytkmktatniyifnlaladalvtttmpfqsavyl 120  
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QY 61 IITAVYSVVFVVGVLGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQSAVYL 120  
|||||

Db 121 mnswpfgdvclckivisidyynmftsifltmmsvdryiavchp vkaldfrt plkakiini 180  
|||||

QY 121 MNSWPFQDVLCCKIVISIDYNNMFTSIFLTMMMSVDRYIAVCHP VKALDFRTPLKAKIINI 180  
|||||

Db 181 ciwllassvgisaivlggtkvredvdiacsqfpddesyswldf mki cvfvfafvipvl 240  
|||||

QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWDLFMKICVVFVFAVIPVL 240  
|||||

Db 241 iivvcytlmilrlksvrlsgsrekdnrlrritklvlvvvavfiicwt pihifilvealg 300  
|||||

QY 241 IIVVCYTLMLRLKSVRLSGSREKDRNLRRITKLVVVVAVFIICWTP IHI FILVEALG 300  
|||||

Db 301 stshstaalssyffcialgytnsslnp vlyafldenfkrcfrdfc fipk mmerqstnrv 360  
|||||

QY 301 STSHSTAALSSYFFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360  
|||||

Db 361 rntvgdpasmrdvvgmnkp v 380  
|||||

QY 361 RNTVQDPASMRDVGGMNKP V 380  
|||||

Query Match 99.6%; Score 2829; DB 14; Length 380;  
Best Local Similarity 98.9%; Pred. No. 6.49e-251;  
Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 mespiqifrgdpgptcpsacllpnssswfnwaesdsgsvgsdqqlsahispaipv 60  
|||||

QY 1 MESPIQIFRGDPGPTCPSACLLPNSSSWFNPWAESDSNGSVGSEDQQLSAHISPAIPV 60  
|||||

Db 61 iitavysvfvvlgvgnslvmfviirytkmktatniyifnlaladalvtttmpfqsavyl 120  
|||||

QY 61 IITAVYSVVFVVGVLGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQSAVYL 120  
|||||

Db 121 mnswpfgdvclckivisidyynmftsifltmmsvdryiavchp vkaldfrt plkakiini 180  
|||||

QY 121 MNSWPFQDVLCCKIVISIDYNNMFTSIFLTMMMSVDRYIAVCHP VKALDFRTPLKAKIINI 180  
|||||

Db 181 ciwllassvgisaivlggtkvredvdiacsqfpddesyswldf mki cvfvfafvipvl 240  
|||||

QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWDLFMKICVVFVFAVIPVL 240  
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Db 241 iivcytlmilrksvrlslsgsrekdrnlrritklvlvvavfiicwtptihifilvealg 300  
QY 241 iivcytlmilrksvrlslsgsrekdrnlrritklvlvvavfiicwtptihifilvealg 300  
Db 301 stshstavlssyyficialgynsslnpvlvfyaldenfkrcfdcfcpikmrmerqstnrv 360  
QY 301 stshstaalssyyficialgynsslnpvlvfyaldenfkrcfdcfcpikmrmerqstnrv 360  
Db 361 rntvqdpasmrdvvggmknkp 380  
QY 361 RNTVQDPASMRDVGGMKNKP 380  
RESULT 4  
ID R72591 standard; Protein; 380 AA.  
AC R72591;  
DT 01-DEC-1995 (first entry)  
DE Mammalian kappa opioid receptor protein.  
KW Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;  
KW amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.  
OS Rattus rattus.  
FH Key Location/Qualifiers  
FT cds 111..1253  
FT /\*tag= a  
FT /product= kappa opioid receptor  
PN J07070191-A.  
PD 14-MAR-1995.  
PF 30-JUL-1993; 190261.  
PR 09-JUL-1993; JP-170591.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
DR WPI; 95-144857/19.  
DR N-PSDB; Q86725.  
PT Kappa opioid receptor protein and cells expressing it - useful  
PT for the screening of compounds for analgesic and hypnotic  
PT properties  
PS Claim 2; Page 9-10; 15pp; Japanese.  
CC The amino acid sequence of the novel mammalian kappa opioid receptor.  
CC The gene was isolated by amplifying a fragment from rat brain mRNA by  
CC reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from  
CC the mouse delta-opioid receptor gene. This fragment was cloned into the  
CC plasmid pCRII to produce pRI1. The plasmid pRI1 was used to probe a rat  
CC brain DNA library in lambda ZAPII to obtain a clone of the rat kappa  
CC opioid receptor gene, designatd pKOPR2. This clone was introduced into  
CC E.coli JM109 for production of the receptor protein. The receptor protein  
CC is useful for screening of analgesic and hypnotic compounds including  
CC peptides and proteins.  
SQ Sequence 380 AA;  
Query Match 99.4%; Score 2823; DB 14; Length 380;  
Best Local Similarity 98.7%; Pred. No. 2.40e-250;  
Matches 375; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
Db 1 mespiqifrgpgeptcapsacllpnssswfpnwaesdngslgsdqglepahispaipv 60  
QY 1 MESPIQIFRGDPGPTCSPSACLLPNSSSWFPNWAESDNGSVGSEDQQLESAHTSPAIPV 60  
Db 61 iitavysvfvvvglgvnslyvmfviirytkmktatniyifnladalavttttmpfqsavyl 120  
QY 61 IITAVYSVVFVVGVLGNSLVMFVIIRYTKMKTATNIYIFNLADALVTTTTPFQSAVYL 120  
Db 121 mnswpfgdvclckivisidynnmftsiftltmmsvryiavchpvpkaldfrtplkakiini 180  
QY 121 MNSWPFEGDVLCKIVISIDYNNMFTSIFTLTMMSVDRIYAVCHPVKALDFRTPLKAKIINI 180  
Db 181 ciwllassvgisaivlggtkvredvdviesclqfpddeyswwdlfmkicvfafvipvl 240  
QY 181 CIWLLASSVGISAIVLGKTKVREDVDVIECSLQFPDDEYSWWDLFMKICVFVFAVIPVL 240  
Db 241 iivcytlmilrksvrlslsgsrekdrnlrritklvlvvavfiicwtptihifilvealg 300  
QY 241 iivcytlmilrksvrlslsgsrekdrnlrritklv-vvvavfiicwtptihifilvealg 300  
Db 301 stshstavlssyyficialgynsslnpvlvfyaldenfkrcfdcfcpikmrmerqstnrv 360

QY 301 STSHSTAALSSYYFICIALGYNSSLNPLVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRY 360  
Db 361 rntvqdpasmrdvvggmknkp 380  
QY 361 RNTVQDPASMRDVGGMKNKP 380  
RESULT 5  
ID W30297 standard; Protein; 380 AA.  
AC W30297;  
DT 14-APR-1998 (first entry)  
DE Human kappa opioid receptor.  
KW Selective target cell activation; G protein-coupled receptor;  
KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;  
KW human; transgenic animal; arrhythmia; bone disease; seizure;  
KW vascular contraction; disease model.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Domain 1..58  
FT /label= N-terminus  
FT /note= "extracellular"  
FT 59..85  
FT /label= TMH1  
FT /note= "transmembrane"  
FT 86..95  
FT /label= I1  
FT /note= "cytoplasmic"  
FT 96..117  
FT /label= TMH2  
FT /note= "transmembrane"  
FT 118..132  
FT /label= E2  
FT /note= "Extracellular"  
FT 133..154  
FT /label= TMH3  
FT /note= "transmembrane"  
FT 155..173  
FT /label= I2  
FT /note= "Cytoplasmic"  
FT 174..196  
FT /label= TMH4  
FT /note= "transmembrane"  
FT 197..222  
FT /label= E2  
FT /note= "extracellular"  
FT 223..247  
FT /label= TMH5  
FT /note= "transmembrane"  
FT 248..275  
FT /label= I3  
FT /note= "Cytoplasmic"  
FT 276..299  
FT /label= TMH6  
FT /note= "Transmembrane"  
FT 300..311  
FT /label= E3  
FT /note= "Extracellular"  
FT 312..333  
FT /label= TMH7  
FT /note= "transmembrane"  
FT 334..380  
FT /label= C-terminus  
FT /note= "cytoplasmic"  
FT Disulfide\_bond 131..210  
FT Modified\_site 25  
FT /note= "potential N-glycosylation"  
FT 39  
FT /note= "potential N-glycosylation"  
FT 345  
FT /note= "palmitate"  
PN W09735478-A1.  
PD 02-OCT-1997.



KW Selective target cell activation; G protein-coupled receptor;  
KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;  
KW human; transgenic animal; arrhythmia; bone disease; seizure;  
KW vascular contraction; disease model.

(REGC ) UNIV CALIFORNIA.  
Conklin BR;  
WPI; 97-502739/46.  
N-PSDB; T90999.  
Selective activation of target cell expressing modified G protein coupled receptor - allows control of cellular proliferation, especially for amplification of transfected cells in gene therapy Example 1; Page 77-79; 117pp; English.  
This polypeptide comprises the human G protein-coupled kappa opiod receptor (KOR) (see also W30297) flanked by N- and C-terminal sequences that facilitate the detection and purification of recombinant KOR, and especially KOR RASSLS (see W30299), i.e. a receptor activated superiorly by a synthetic ligand. A novel method for selectively activating a target cell (TC) comprises: (i) introducing into the cell a nucleic acid sequence (I) that expresses a RASSL (A) and (ii) exposing the transfected cell to small synthetic molecules (B) that bind to and activate (A), inducing the G protein coupled cellular response associated with receptor activation. (A) has: (a) decreased binding affinity for a selected natural ligand of the native receptor; (b) binding affinity for (B); and (c) is activated by binding (B) sufficiently to produce the required cellular response. Also new are: transgenic cells including heterologous (I) in the genome; cellular implants comprising a TC transfected with (I); isolated (I); and transgenic animals expressing (A). Activation of (A) results, in vitro or in vivo, in cellular proliferation, or secretion of a cellular product, particularly a heterologous therapeutic protein encoded by a second inserted nucleic acid sequence. Particularly it is used to expand the relatively few cells that are successfully transfected during gene therapy procedures. Other responses that can be regulated are cell migration and contraction, or pigment production. In transgenic animals, expression or stimulation of (A) is designed to develop cardiac arrhythmia, symptoms of bone disease, seizures, vascular contractions, dementia, neurodegeneration etc., for use as models of these diseases (claimed). The transgenic animals are also used for production of improved food products (e.g. increased calcium content in eggshells or altered fat/lean ratios) or to control fertility or induce labour.  
Sequence 427 AA;

```
RESULT      8
ID    W30299 standard; Protein; 424 AA.
AC    W30299;
DI    14-APR-1998 (first entry)
DE    Human kappa opioid receptor RASSL ORL.
KW    Selective target cell activation; G protein-coupled receptor;
KW    RASSL; gene therapy; cell proliferation; kappa opioid receptor;
KW    human; transgenic animal; arrhythmia; bone disease; seizure;
KW    vascular contraction; disease model.
OS    Chimeric - Homo sapiens.
FH    Chimeric - Synthetic.
FT    key      Location/Qualifiers
FT    Peptide  1..30
FT              /label= Sig_peptide
FT              /note= "prolactin signal sequence"
FT    Peptide  31..38
FT              /label= FLAG
FT    Protein  39..414
FT              /label= KOR
FT              /note= "human kappa opioid receptor"
FT    Domain   39..95
FT              /label= N-terminus
FT              /note= "extracellular"
FT    Domain   96..122
FT              /label= TMH1
FT              /note= "transmembrane"
FT    Domain   123..132
FT              /label= I1
FT              /note= "cytoplasmic"
FT    Domain   133..154
FT              /label= TMH2
FT              /note= "transmembrane"
FT    Domain   155..169
FT              /label= E2
FT              /note= "Extracellular"
FT    Domain   170..191
FT              /label= TMH3
FT              /note= "transmembrane"
FT    Domain   192..210
FT              /label= I2
FT              /note= "Cytoplasmic"
FT    Domain   211..233
FT              /label= TMH4
FT              /note= "transmembrane"
FT    Domain   234..259
FT              /label= E2
FT              /note= "extracellular, contains 17 amino acid
FT              residues from delta opiod receptor
FT              (Val-235, Gln-237, Pro-238, Asp-240,
FT              Gly-241, Ala-242, Val-243, Val-244,
FT              Thr-246, Ser-251, Pro-252, Ser-253,
FT              Trp-254, Tyr-255, Thr-258, Val-259,
FT              Thr-260)"
FT    Domain   260..281
FT              /label= TMH5
FT              /note= "transmembrane"
FT    Domain   282..309
FT              /label= I3
FT              /note= "Cytoplasmic"
FT    Domain   310..333
FT              /label= TMH6
FT              /note= "Transmembrane"
FT    Domain   334..345
FT              /label= E3
FT              /note= "Extracellular"
FT    Domain   346..367
FT              /label= TMH7
FT              /note= "transmembrane"
FT    Domain   368..414
FT              /label= C-terminus
FT              /note= "cytoplasmic"
FT    Disulfide_bond 168..245
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FT    Modified_site 62
FT              /note= "potential N-glycosylation"
FT    Modified_site 76
FT              /note= "potential N-glycosylation"
FT    Modified_site 382
FT              /note= "palmitate"
FT    Peptide      415..424
FT              /label= HA
PN    WO9735478-A1.
PD    02-OCT-1997.
PF    25-MAR-1997; U05334.
PR    26-MAR-1996; US-622348.
PA    (REGC ) UNIV CALIFORNIA.
PI    Conklin BR;
DR    WPI; 97-502739/46.
DR    N-PSDB; T92601.
PT    Selective activation of target cell expressing modified G protein
PT    coupled receptor - allows control of cellular proliferation,
PT    especially for amplification of transfected cells in gene therapy
PT    Example 1; Page 80-82; 117pp; English.
PS    This protein comprises RASSL ORL, a G protein-coupled receptor that
CC    is activated superiorly by synthetic ligands. ORL comprises human
CC    G protein-coupled kappa opioid receptor (KOR) (see also W30297)
CC    modified at 17 amino acid positions to contain the corresponding
CC    amino acid of the delta opioid receptor, and containing N- and
CC    C-terminal flanking sequences that facilitate the detection and
CC    purification of recombinant protein. A novel method for selectively
CC    activating a target cell (TC) comprises: (i) introducing into the
CC    cell a nucleic acid sequence (I) (see T92601) that expresses a RASSL
CC    (A) and (ii) exposing the transfected cell to small synthetic molecules
CC    (B) that bind to and activate (A), inducing the G protein coupled
CC    cellular response associated with receptor activation. (A) has: (a)
CC    decreased binding affinity for a selected natural ligand of the
CC    native receptor; (b) binding affinity for (B); and (c) is activated
CC    by binding (B) sufficiently to produce the required cellular response.
CC    Also new are: transgenic cells including heterologous (I) in the
CC    genome; cellular implants comprising a TC transfected with (I);
CC    isolated (I); and transgenic animals expressing (A). Activation of
CC    (A) results, in vitro or in vivo, in cellular proliferation, or
CC    secretion of a cellular product, particularly a heterologous
CC    therapeutic protein encoded by a second inserted nucleic acid
CC    sequence. Particularly it is used to expand the relatively few
CC    cells that are successfully transfected during gene therapy
CC    procedures. Other responses that can be regulated are cell
CC    migration and contraction, or pigment production. In transgenic
CC    animals, expression or stimulation of (A) is designed to develop
CC    cardiac arrhythmia, symptoms of bone disease, seizures, vascular
CC    contractions, dementia, neurodegeneration etc., for use as models
CC    of these diseases (claimed). The transgenic animals are also used
CC    for production of improved food products (e.g. increased calcium
CC    content in eggshells or altered fat/lean ratios) or to control
CC    fertility or induce labour.
SQ    Sequence 424 AA;
```

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Query Match      90.1%; Score 2559; DB 27; Length 424;
Best Local Similarity 89.2%; Pred. No. 2.29e-225;
Matches 340; Conservative 20; Mismatches 16; Indels 5; Gaps 4;
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Db    38 vdsplqifrgpgptcapsaclppnssawfpgwaepdngsagsdaqlpahispaipv 97
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY    1 MESPIQIFRGDPGPTCSPSACLLPNSSWFPNWAESDSNGSVGSEDDQLESAHISPAIPV 60

Db    98 itavysvfvvglvgnslvmfvliirytkmktatniyifnlaladalvttmpfqstvy 157
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY    61 IITAVISVVFVVGVLVGNLSLMFVIIRYTKMKTATNIYIFNLALADALVTTMPFQSAVYL 120

Db    158 mnswpfgdvlickivisidynnfmftsiftlmmssvdryiavchp vkaldfrt plkakiini 217
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY    121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMMMSVDRIYAVCHP VKALDFRTPLKAKIINI 180

Db    218 ciwllassvgisai vlgvtqprdga-vv-ctlqfssp--swywdvtvkicvfifavipv 273
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY    181 CIWLLASSVGISAI VLGTVKREDVDVIECSLQFPDDEYSW-WDLFMKICVVFVFAFVIPV 239
```



QY 156 RYIAVCHPVKALDFRTPKAKIINICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFP 215

Db 181 hptw-ywenllkicvfafimpvliitvcyglmrlksvrmllsgskekdrlrritrm 239

QY 216 DDEYSWDLFMKICVFVAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRAITKL 275

Db 240 vlvvvavfivcwtptihyvikalitipettftqtswhficialgytnsclnppvlyafide 299

QY 276 VLVVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPNVLYAFIDE 335

Db 300 nfkrcfrefciptsstieqgnstrvrqntrehpstantv 338

QY 336 NFKRCFRDFCFPIKMRMERQSTNVR-NTVQDPASMRDV 373

RESULT 11

ID W44937 standard; Protein; 398 AA.

AC W44937;

DI 28-OCT-1998 (first entry)

DE Mouse mu opiate receptor.

KW Mouse; mu opiate receptor; transgenic animal; mammal; identification;

KW exon; nervous tissue; pain; drug addiction; transplant rejection;

KW immunosuppressant; analgesic; morphine; side effect.

OS Mus sp.

PN WO9802534-A2.

PD 22-JAN-1998.

PF 11-JUL-1997; F01282.

PR 15-JUL-1996; FR-008810.

PA (CNRS ) CENT NAT RECH SCI.

PI Dierich A, Kieffer BL, LeMeur M, Matthes HWD, Simonin FH;

DR WPI; 98-110582/10.

DR N-PSDB; V49252.

PT Transgenic animals defective in one type of opioiid receptor - used

PT to identify agents for treatment of pain, drug addiction and

PT transplant rejection, lacking side effects of known opiate(s)

PS Disclosure; Fig 11; 58pp; French.

CC This sequence represents the mouse mu opiate receptor. The gene sequence

CC is used to generate a transgenic non-human mammal for identifying agents

CC for treating disorders associated with opiate receptors. In the mammal,

CC the expression of the gene encoding the opiate receptor is modified,

CC particularly by the deletion of an exon and/or insertion of a marker

CC gene, e.g. the neomycin resistance gene, into the sequence. Especially

CC the expression of the gene is altered in nervous tissue. The agents are

CC potentially useful for treating severe pain (chronic or acute), drug

CC addiction and/or prevention or treatment of transplant rejection (as

CC immunosuppressants). The method may isolate and identify powerful

CC analgesics that lack morphine-like side effects.

SQ Sequence 398 AA;

Query Match 59.1%; Score 1678; DB 34; Length 398;

Best Local Similarity 65.8%; Pred. No. 2.77e-142;

Matches 208; Conservative 55; Mismatches 49; Indels 4; Gaps 4;

Db 68 aitimalysivcvglfgnflvmyvivrytkmktatniyifnladalatstlpfqswn 127

QY 59 PVIIITAVYSVVFVVGVLVGNLSLVMFVRIIRYTKMKTATNIYIFNLADALVTTTTPFQSAY 118

Db 128 ylmgtwpgfnilckivisidynnfmftsiftlctmsvdryiavchpvcaldfrtprnakiv 187

QY 119 YLMNSWPFGDLCKIVISIDYNNMFTSIFTLTMSVDRYIAVCHPVKALDFRTPLKAKII 178

Db 188 nvcnwilssaiqlpvmfmattkkyrqg-s-idctltfshptw-ywenllkicvfifafimp 244

QY 179 NICIWLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFVIP 238

Db 245 vliitvcyglmrlksvrmllsgskekdrlrritrmvlvvavfivcwtptihyviika 304

QY 239 VLIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVVAVFIIICWTPIHIFILVEA 298

Db 305 litipettftqtswhficialgytnsclnppvlyafldenfkrcfrefciptsstieqnsa 364

QY 299 LGSTSHSTAALSSYYFCIALGYTNSSLNPNVLYAFLDENFKRCFRDFCFPIKMRMEROSTN 358

QY 156 RYIAVCHPVKALDFRTPKAKIINICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFP 215

Db 181 hptw-ywenllkicvfafimpvliitvcyglmrlksvrmllsgskekdrlrritrm 239

QY 216 DDEYSWDLFMKICVFVAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRAITKL 275

Db 240 vlvvvavfivcwtptihyvikalitipettftqtswhficialgytnsclnppvlyafide 299

QY 276 VLVVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPNVLYAFIDE 335

Db 300 nfkrcfrefciptsstieqgnstrvrqntrehpstantv 338

QY 336 NFKRCFRDFCFPIKMRMERQSTNVR-NTVQDPASMRDV 373

RESULT 12

ID R71966 standard; Protein; 400 AA.

AC R71966;

DT 20-OCT-1995 (first entry)

DE Human mu opioiid receptor.

KW Mu opioiid receptor; MOR; gene therapy; diagnostic.

OS Homo sapiens.

PN WO9507983-A.

PD 23-MAR-1995.

PF 13-SEP-1994; U10358.

PR 13-SEP-1993; US-120601.

PA (INDV ) UNIV INDIANA FOUND.

PI Yu L;

DR WPI; 95-131351/17.

DR N-PSDB; Q89226.

PT New nucleic acid encoding new human mu opioiid receptor - and

PT related vectors, transformed cells, antibodies etc., useful in

PT diagnosis, treatment and drug screening.

PS Claim 4; Page 211-214; 266pp; English.

CC A cDNA library constructed from human caudate nucleus mRNA was

CC screened with rat mu opioiid receptor cDNA under conditions of

CC low stringency. One positive clone included the sequence given in

CC Q89226, encoding a mu opioiid receptor MOR (R71964). The cDNA

CC is used for prodn. of recombinant MOR, in gene therapy, etc.

SQ Sequence 400 AA;

Query Match 59.1%; Score 1677; DB 13; Length 400;

Best Local Similarity 66.6%; Pred. No. 3.44e-142;

Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

Db 70 aitimalysivcvglfgnflvmyvivrytkmktatniyifnladalatstlpfqswn 129

QY 59 PVIIITAVYSVVFVVGVLVGNLSLVMFVRIIRYTKMKTATNIYIFNLADALVTTTTPFQSAY 118

Db 130 ylmgtwpgftilckivisidynnfmftsiftlctmsvdryiavchpvcaldfrtprnakii 189

QY 119 YLMNSWPFGDLCKIVISIDYNNMFTSIFTLTMSVDRYIAVCHPVKALDFRTPLKAKII 178

Db 190 nvcnwilssaiqlpvmfmattkkyrqg-s-idctltfshptw-ywenllkicvfifafimp 246

QY 179 NICIWLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFVIP 238

Db 247 vliitvcyglmrlksvrmllsgskekdrlrritrmvlvvavfivcwtptihyviika 306

QY 239 VLIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVVAVFIIICWTPIHIFILVEA 298

Db 307 lvtipettftqtswhficialgytnsclnppvlyafldenfkrcfrefciptsstieqgnst 366

QY 299 LGSTSHSTAALSSYYFCIALGYTNSSLNPNVLYAFLDENFKRCFRDFCFPIKMRMERQSTN 358

Db 367 rirqntdrhps 377

QY 359 RVRNTVQDPAS 369

RESULT 13

ID R76781 standard; Protein; 398 AA.

AC R76781;

DT 11-DEC-1995 (first entry)

DE Rat mu opiate receptor.

KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;

KW drug abuse; analgesic.

OS Rattus sp.

PN WO9520667-A1.

PD 03-AUG-1995.

PF 30-JAN-1995; U01144.

PR 28-JAN-1994; US-188275.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Db 365 rirqntrehpstantv 380

QY 359 RVR-NTVQDPASMRDV 373

RESULT 12

ID R71966 standard; Protein; 400 AA.

AC R71966;

DT 20-OCT-1995 (first entry)

DE Human mu opioiid receptor.

KW Mu opioiid receptor; MOR; gene therapy; diagnostic.

OS Homo sapiens.

PN WO9507983-A.

PD 23-MAR-1995.

PF 13-SEP-1994; U10358.

PR 13-SEP-1993; US-120601.

PA (INDV ) UNIV INDIANA FOUND.

PI Yu L;

DR WPI; 95-131351/17.

DR N-PSDB; Q89226.

PT New nucleic acid encoding new human mu opioiid receptor - and

PT related vectors, transformed cells, antibodies etc., useful in

PT diagnosis, treatment and drug screening.

PS Claim 4; Page 211-214; 266pp; English.

CC A cDNA library constructed from human caudate nucleus mRNA was

CC screened with rat mu opioiid receptor cDNA under conditions of

CC low stringency. One positive clone included the sequence given in

CC Q89226, encoding a mu opioiid receptor MOR (R71964). The cDNA

CC is used for prodn. of recombinant MOR, in gene therapy, etc.

SQ Sequence 400 AA;

Query Match 59.1%; Score 1677; DB 13; Length 400;

Best Local Similarity 66.6%; Pred. No. 3.44e-142;

Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

Db 70 aitimalysivcvglfgnflvmyvivrytkmktatniyifnladalatstlpfqswn 129

QY 59 PVIIITAVYSVVFVVGVLVGNLSLVMFVRIIRYTKMKTATNIYIFNLADALVTTTTPFQSAY 118

Db 130 ylmgtwpgftilckivisidynnfmftsiftlctmsvdryiavchpvcaldfrtprnakii 189

QY 119 YLMNSWPFGDLCKIVISIDYNNMFTSIFTLTMSVDRYIAVCHPVKALDFRTPLKAKII 178

Db 190 nvcnwilssaiqlpvmfmattkkyrqg-s-idctltfshptw-ywenllkicvfifafimp 246

QY 179 NICIWLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFVIP 238

Db 247 vliitvcyglmrlksvrmllsgskekdrlrritrmvlvvavfivcwtptihyviika 306

QY 239 VLIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVVAVFIIICWTPIHIFILVEA 298

Db 307 lvtipettftqtswhficialgytnsclnppvlyafldenfkrcfrefciptsstieqgnst 366

QY 299 LGSTSHSTAALSSYYFCIALGYTNSSLNPNVLYAFLDENFKRCFRDFCFPIKMRMERQSTN 358

Db 367 rirqntdrhps 377

QY 359 RVRNTVQDPAS 369

RESULT 13

ID R76781 standard; Protein; 398 AA.

AC R76781;

DT 11-DEC-1995 (first entry)

DE Rat mu opiate receptor.

KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;

KW drug abuse; analgesic.

OS Rattus sp.

PN WO9520667-A1.

PD 03-AUG-1995.

PF 30-JAN-1995; U01144.

PR 28-JAN-1994; US-188275.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.



```
CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. Expression
CC of hMOR1 in COS cells revealed high affinity recognition of the mu
CC opiate specific ligand. Recombinant hMOR1 can be used to screen
CC compounds for analgesic activity.
SQ Sequence 400 AA;

Query Match 59.0%; Score 1675; DB 14; Length 400;
Best Local Similarity 66.6%; Pred. No. 5.30e-142;
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

Db 70 aitimalyslvcvvglfngflvmyvivrytkmktatniyifnlaladalatstlpfqsvn 129
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 59 PVIITAVYSVVFVVGVLVGNLSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAV 118

Db 130 ylmgtwpgtilckivisidynnftsiftlctmsvdryiavchpvkaldfrtprnakii 189
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 119 YLMNSWPFQGVLCIKIVISIDYNNMFTSIFTLTMMMSVDRIYAVCHPVKALDFRTPKAKII 178

Db 190 nvcnwilssaiglpvmfmatkkyrgg-s-idctltfshptw-ywenlvkicvfifafimp 246
   | :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 179 NICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWWDLEMKICVVFVAFVIP 238

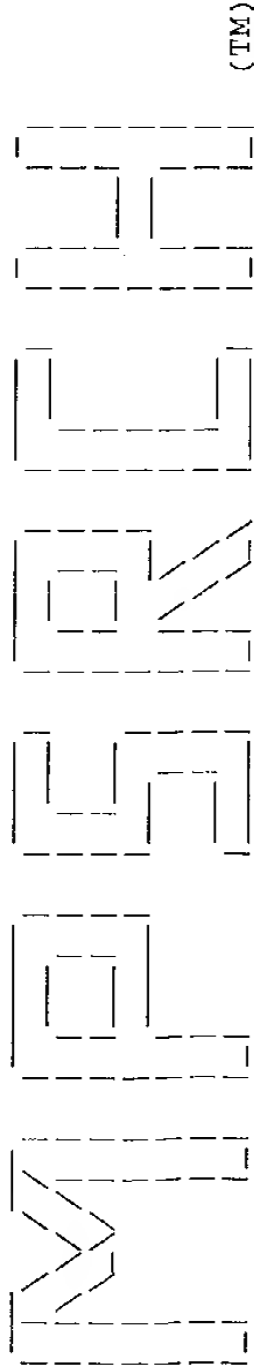
Db 247 vliitvcyglmilrlksvrmlsgskekdnlrritrmvlvvavfvcwtpihiyviika 306
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :|
QY 239 VLIIVCYTLMILRLKSVRLLSGSRKEDNLRRTKLVLVVAVFIICWTPIHIFILVEA 298

Db 307 lvtipettftqsvwhficialgytnsclnpvlyafldenfkrcfrefcipcptsnieqnst 366
   | : : | | | | | | | | | | | | | | | | | | | | | | | | | | :| :|
QY 299 LGSTSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTN 358

Db 367 rirgntrdhps 377
   | : | : | : |
QY 359 RVRNTVQDPAS 369
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Search completed: Thu Feb 17 11:12:04 2000  
Job time : 28 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit.  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Feb 17 11:14:24 2000; MasPar time 8.92 Seconds  
Tabular output not generated. 552.170 Million cell updates/sec

Title: >US-08-455-683-2  
Description: (1-380) from US08455683.pep  
Perfect Score: 2839  
Sequence: 1 MESPIQIFRGDPGPTCPSA.....RNTVQDPASMRDVGGMKPV 380

Scoring table: PAM 150  
Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 32.927; Variance 157.770; scale 0.209

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2826	99.5	380	1	US-08-149-Sequence 7, Applicatio	3.11e-238
2	2826	99.5	380	2	US-08-911-Sequence 7, Applicatio	3.11e-238
3	2685	94.6	378	2	US-08-514-Sequence 10, Applicati	1.39e-225
4	1887	66.5	330	2	US-08-454-Sequence 5, Applicatio	3.75e-154
5	1677	59.1	400	3	PCT-US94-1Sequence 8, Applicatio	2.03e-135
6	1676	59.0	391	2	US-08-454-Sequence 3, Applicatio	2.50e-135
7	1674	59.0	398	3	PCT-US94-1Sequence 5, Applicatio	3.76e-135
8	1674	59.0	398	1	US-08-149-Sequence 5, Applicatio	3.76e-135
9	1674	59.0	398	2	US-08-911-Sequence 5, Applicatio	3.76e-135
10	1610	56.7	367	2	US-08-454-Sequence 4, Applicatio	1.89e-129
11	1598	56.3	372	2	US-08-411-Sequence 2, Applicatio	2.22e-128
12	1597	56.3	372	2	US-08-411-Sequence 10, Applicati	2.72e-128
13	1593	56.1	372	2	US-08-911-Sequence 6, Applicatio	6.18e-128
14	1593	56.1	372	1	US-08-149-Sequence 6, Applicatio	6.18e-128
15	1574	55.4	398	2	US-08-514-Sequence 8, Applicatio	3.04e-126
16	1485	52.3	372	2	US-08-514-Sequence 9, Applicatio	2.52e-118
17	1473	51.9	367	3	PCT-US94-1Sequence 17, Applicati	2.94e-117
18	1473	51.9	367	2	US-08-454-Sequence 2, Applicatio	2.94e-117
19	1444	50.9	367	1	US-08-149-Sequence 4, Applicatio	1.11e-114
20	1444	50.9	367	2	US-08-553-Sequence 4, Applicatio	1.11e-114
21	1444	50.9	367	2	US-08-514-Sequence 4, Applicatio	1.11e-114
22	1444	50.9	367	2	US-08-911-Sequence 4, Applicatio	1.11e-114
23	1336	47.1	367	2	US-08-514-Sequence 7, Applicatio	4.35e-105

24	1195	42.1	367	1	US-08-147-Sequence 2, Applicatio	1.36e-92
25	980	34.5	391	1	US-07-816-Sequence 4, Applicatio	1.31e-73
26	980	34.5	391	1	US-08-417-Sequence 4, Applicatio	1.31e-73
27	976	34.4	391	1	US-08-417-Sequence 14, Applicati	2.95e-73
28	976	34.4	391	1	US-08-417-Sequence 2, Applicatio	2.95e-73
29	976	34.4	391	1	US-07-816-Sequence 2, Applicatio	2.95e-73
30	927	32.7	369	2	US-08-411-Sequence 3, Applicatio	6.04e-69
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32	922	32.5	369	1	US-08-417-Sequence 8, Applicatio	1.66e-68
33	912	32.1	369	1	US-08-417-Sequence 16, Applicati	1.26e-67
34	912	32.1	369	1	US-08-417-Sequence 6, Applicatio	1.26e-67
35	912	32.1	369	1	US-07-816-Sequence 6, Applicatio	1.26e-67
36	850	29.9	333	1	US-08-148-Sequence 4, Applicatio	3.47e-62
37	817	28.8	322	3	PCT-US93-0Sequence 75, Applicati	2.70e-59
38	817	28.8	322	1	US-08-118-Sequence 75, Applicati	2.70e-59
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41	792	27.9	328	1	US-08-148-Sequence 2, Applicatio	4.15e-57
42	732	25.8	428	1	US-08-417-Sequence 12, Applicati	7.19e-52
43	732	25.8	428	1	US-07-816-Sequence 12, Applicati	7.19e-52
44	630	22.2	211	2	US-08-771-Sequence 19, Applicati	5.27e-43
45	630	22.2	211	1	US-07-915-Sequence 19, Applicati	5.27e-43

ALIGNMENTS

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DE  
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DE  
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Sequence 7, Application US/08149093A

Sequence 7, Application US/08149093A  
Patent No. 5658783  
GENERAL INFORMATION:

APPLICANT: Bunzow, James R

APPLICANT: Grandy, David K

TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific

TITLE OF INVENTION: Opioid Receptor Gene and Uses

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,093A

FILING DATE: 06-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5658783nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,311

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 380 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

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CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..380
CC OTHER INFORMATION: /label= Identifier
CC OTHER INFORMATION: /note= "Mouse Kappa-Opioid Receptor"
CC SEQUENCE 380 AA; 42652 MW; 802929 CN;

Query Match 99.5%; Score 2826; DB 1; Length 380;
Best Local Similarity 99.5%; Pred. No. 3.11e-238;
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 MESPIQIFRGDPGPTCSPSACLLPNSSWFPNWAESDNGSVGSEDQQLSAHISPAIPV 60
QY |||||
1 MESPIQIFRGDPGPTCSPSACLLPNSSWFPNWAESDNGSVGSEDQQLSAHISPAIPV 60

Db 61 IITAVYSVVFVVGVLGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTMPFQSAVYL 120
QY |||||
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Db 121 MNSWPFQDVLCCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180
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Db 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWWDLFMKICVFVFAFVIPVL 240
QY |||||
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QY |||||
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Db 301 STSHSTAALSSYYFCAILGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360
QY |||||
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Db 361 RNTVQDPASMRDVGGMNKPV 380
QY |||||
361 RNTVQDPASMRDVGGMNKPV 380

RESULT 2
ID US-08-911-245-7 STANDARD; PRT; 380 AA.
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AC xxxxxx
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DT
XX
DE
XX
CC Sequence 7, Application US/08911245
CC Sequence 7, Application US/08911245
CC Patent No. 5821067
CC GENERAL INFORMATION:
CC APPLICANT: Bunzow, James R
CC APPLICANT: Grandy, David K
CC TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
CC TITLE OF INVENTION: Opioid Receptor Gene and Uses
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Banner & Allegretti, Ltd.
CC STREET: 10 South Wacker Drive, Suite 3000
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/911,245
CC FILING DATE: 15-AUG-1997
CC CLASSIFICATION: 536
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CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/149093
CC FILING DATE: 06-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5821067nan, Kevin E
CC REGISTRATION NUMBER: 35,303
CC REFERENCE/DOCKET NUMBER: 93,311
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-715-1000
CC TELEFAX: 312-715-1234
CC TELEX: 910-221-5317
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 380 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..380
CC OTHER INFORMATION: /label= Identifier
CC OTHER INFORMATION: /note= "Mouse Kappa-Opioid Receptor"
CC SEQUENCE 380 AA; 42652 MW; 802929 CN;

Query Match 99.5%; Score 2826; DB 2; Length 380;
Best Local Similarity 99.5%; Pred. No. 3.11e-238;
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 MESPIQIFRGDPGPTCSPSACLLPNSSWFPNWAESDNGSVGSEDQQLSAHISPAIPV 60
QY |||||
1 MESPIQIFRGDPGPTCSPSACLLPNSSWFPNWAESDNGSVGSEDQQLSAHISPAIPV 60

Db 61 IITAVYSVVFVVGVLGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTMPFQSAVYL 120
QY |||||
61 IITAVYSVVFVVGVLGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTMPFQSAVYL 120

Db 121 MNSWPFQDVLCCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180
QY |||||
121 MNSWPFQDVLCCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180

Db 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWWDLFMKICVFVFAFVIPVL 240
QY |||||
181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWWDLFMKICVFVFAFVIPVL 240

Db 241 IIVCYTLMILRLKSVRLLSGSRKDRNLRRITKLVLVVVAVFIICWTPIHIFILVEALG 300
QY |||||
241 IIVCYTLMILRLKSVRLLSGSRKDRNLRRITKLVLVVVAVFIICWTPIHIFILVEALG 300

Db 301 STSHSTAALSSYYFCAILGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360
QY |||||
301 STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360

Db 361 RNTVQDPASMRDVGGMNKPV 380
QY |||||
361 RNTVQDPASMRDVGGMNKPV 380

RESULT 3
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DE
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CC Sequence 10, Application US/08514451A
CC Sequence 10, Application US/08514451A
CC Patent No. 5837809
CC GENERAL INFORMATION:
CC APPLICANT: Bunzow, James R.
CC APPLICANT: Grandy, David K.
CC APPLICANT: Civelli, Olivier
CC APPLICANT: Reinscheid, Rainer K.
```

APPLICANT: NO. 5837809hacker, Hans-Peter  
 APPLICANT: Monsma, Frederick J.  
 TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID  
 TITLE OF INVENTION: RECEPTOR LIGAND AND USES  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klarquist Sparkman Campbell  
 ADDRESSEE: Leigh & Whinston LLP  
 STREET: 121 S.W. Salmon, Suite 1600  
 CITY: Portland  
 STATE: Oregon  
 COUNTRY: USA  
 ZIP: 97204  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WPS.1 ASCII text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/514,451A  
 FILING DATE: 08/11/95  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/553,058  
 FILING DATE: 11/13/95  
 ATTORNEY/AGENT INFORMATION:  
 NAME: William D. No. 5837809nan, M.D.  
 REGISTRATION NUMBER: 30,878  
 REFERENCE/DOCKET NUMBER: 899-45995/WDN  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (503) 226-7391  
 TELEFAX: (503) 228-9446  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 378 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 DESCRIPTION: peptide  
 SEQUENCE 378 AA: 42392 MW: 806199 CN:

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DT  
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CC Sequence 5, Application US/08454549  
CC Sequence 5, Application US/08454549  
CC Patent No. 5866324  
CC GENERAL INFORMATION:  
CC APPLICANT: EPPLER, C. Mark  
CC APPLICANT: OZENBERGER, Bradley A.  
CC APPLICANT: HULMES, Jeffrey D.  
CC TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED  
CC TITLE OF INVENTION: TO OPIOID RECEPTORS  
CC NUMBER OF SEQUENCES: 13  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Darby & Darby, P.C.  
CC STREET: 805 Third Avenue  
CC CITY: New York  
CC STATE: New York  
CC COUNTRY: USA  
CC ZIP: 10022  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/454,549  
CC FILING DATE: 30-MAY-1995  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robinson, Joseph R.  
CC REGISTRATION NUMBER: 33,448  
CC REFERENCE/DOCKET NUMBER: 0646/LA818-US5  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (212) 527-7700  
CC TELEFAX: (212) 753-6237  
CC TELEX: 236687  
CC INFORMATION FOR SEQ ID NO: 5:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 330 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: not relevant  
CC TOPOLOGY: not relevant  
CC MOLECULE TYPE: protein  
CC ORIGINAL SOURCE:  
CC ORGANISM: Rat  
SQ SEQUENCE 330 AA; 36851 MW; 611728 CN;

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QY	241	IIIVCYTLMILRLKSVLLSGSREKDRNLRRITKLVVVVAVFIICWTPIHIFILVEALG	300	
Db	299	STSHSTAALSSYYFCIALGYTMSSLMPVLYAFLDKNFKRCTRDFCFPIKMRMERQSTNRY	358	
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Db	359	RNTVQDPASMRDVGGMNKPV	378	
QY	361	RNTVQDPASMRDVGGMNKPV	380	

Db	191	IIIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVLVVVAVFIICWTPIHIFILVEALG	250
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Db	251	STSHSTAVLSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV	310
QY	301	STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV	360
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CC	Sequence 8, Application PC/TUS9410358		
CC	GENERAL INFORMATION:		
CC	APPLICANT:		
CC	TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS		
CC	NUMBER OF SEQUENCES: 17		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Arnold, White & Durkee		
CC	STREET: P. O. Box 4433		
CC	CITY: Houston		
CC	STATE: Texas		
CC	COUNTRY: USA		
CC	ZIP: 77210		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII		
CC	SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: PCT/US94/10358		
CC	FILING DATE: Concurrently herewith		
CC	CLASSIFICATION:		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: 08/120,601		
CC	FILING DATE: 13 SEPTEMBER 1993		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: WILSON, MARK B.		
CC	REGISTRATION NUMBER: 37,259		
CC	REFERENCE/DOCKET NUMBER: INDA005P--		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: (512) 418-3000		
CC	TELEFAX: (713) 789-2679		
CC	TELEX: 79-0924		
CC	INFORMATION FOR SEQ ID NO: 8:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 400 amino acids		
CC	TYPE: amino acid		
CC	TOPOLOGY: linear		
CC	MOLECULE TYPE: protein		
SQ	SEQUENCE 400 AA; 44779 MW; 873826 CN;		
Query Match			
Best local similarity 66.6%; Pred. No. 2,03e-135;			
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;			
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QY	59	PVIITAVYSVVFVGLVGNLSLVMFVIIRYTKMTATNIYIFNLALADALVTTMPFQSAV	118
Db	130	YLMGTWPFGTILCKIVISIDYNNMFTSIFTLTCTMSVDRIYAVCHPVKALDERTPRNAKII	189
:    :      :      :      :      :      :      :      :			
QY	119	YLMNSWPFGLVCKIVISIDYNNMFTSIFTLTCTMSVDRIYAVCHPVKALDERTPLKAKII	178
Db	190	NVCNWILSSAIGLPVMEWATKYRQG-S-IDCILTFSHPTW-YWENLLKICVFIEFALMP	246
QY	179	NICIWLLASSVGISAIVLGGTKVREDVDVIECSLOFPDDEYSWWDLFMKICVFVFAFVIP	238
Db	247	VLIITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMLVVLVVAVFIVCWTPIHIYVILKA	306
QY	239	VLIITVCYTLMLRLKSVRLSGSREKDRNLRRITKLVLVVVAVFIICWTPIHIFILVEA	298
Db	307	LVTIPETTFQTVSWHFCIALGYTNSSLNPVLYAFLDENFKRCFRFECIPTSSNIEQQNST	365
QY	299	LGSTSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTN	358
Db	367	RIRQNRDHP	377
QY	359	RVRNIVQDPAS	369
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XX	xxxxxx		
DE	Sequence 3, Application US/08454549		
CC	Sequence 3, Application US/08454549		
CC	Patent No. 5866324		
CC	GENERAL INFORMATION:		
CC	APPLICANT: EPPLER, C. Mark		
CC	APPLICANT: OZENBERGER, Bradley A.		
CC	APPLICANT: HULMES, Jeffrey D.		
CC	TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED		
CC	TITLE OF INVENTION: TO OPIOID RECEPTORS		
CC	NUMBER OF SEQUENCES: 13		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Darby & Darby, P.C.		
CC	STREET: 805 Third Avenue		
CC	CITY: New York		
CC	STATE: New York		
CC	COUNTRY: USA		
CC	ZIP: 10022		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: Patentin Release #1.0, Version #1.30		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/454,549		
CC	FILING DATE: 30-MAY-1995		
CC	CLASSIFICATION: 435		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Robinson, Joseph R.		
CC	REGISTRATION NUMBER: 33,448		
CC	REFERENCE/DOCKET NUMBER: 0646/1A818-US5		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: (212) 527-7700		
CC	TELEFAX: (212) 753-6237		
CC	TELEX: 236687		
CC	INFORMATION FOR SEQ ID NO: 3:		
CC	SEQUENCE CHARACTERISTICS:		
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CC	TYPE: amino acid		
CC	STRANDEDNESS: not relevant		
CC	TOPOLOGY: not relevant		
CC	MOLECULE TYPE: protein		
CC	ORIGINAL SOURCE:		
CC	ORGANISM: Rat		
SQ	SEQUENCE 391 AA; 43814 MW; 846718 CN;		
Query Match			
59.0%; Score 1676; DB 2; Length 391;			





CC NUMBER OF SEQUENCES: 13  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Darby & Darby, P.C.  
CC STREET: 805 Third Avenue  
CC CITY: New York  
CC STATE: New York  
CC COUNTRY: USA  
CC ZIP: 10022  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC FILING DATE: 30-MAY-1995  
CC APPLICATION NUMBER: US/08/454,549  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robinson, Joseph R.  
CC REGISTRATION NUMBER: 33,448  
CC REFERENCE/DOCKET NUMBER: 0646/1A818-US5  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (212) 527-7700  
CC TELEFAX: (212) 753-6237  
CC TELEX: 236687  
CC INFORMATION FOR SEQ ID NO: 4:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 367 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: not relevant  
CC TOPOLOGY: not relevant  
CC MOLECULE TYPE: protein  
CC ORIGINAL SOURCE:  
CC ORGANISM: Rat  
SQ SEQUENCE 367 AA; 40122 MW; 712609 CN;

Query Match 56.7%; Score 1610; DB 2; Length 367;  
Best Local Similarity 65.6%; Pred. No. 1.89e-129;  
Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;

Db 15 LLANVSDTFPSAFPSASANASGSPGAR--SAS-SLALAIAITALYSACVAVGLGNVLVM 71  
QY 22 LLPNSSWFNPWAESDSNGSVGSEDDQLESAAHISPAIPVIITAVISVVFVGLVGNLSVM 81  
Db 72 FGIVRYTKLKTATNIYIFNLALADALAIATLTPFQSAKYLMETWPFGEILLCKAVLSIDYIN 131  
QY 82 FVIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAVYLMNSWPFQDVLCKIVISIDYIN 141  
Db 132 MFTSIFTLTMMSVDRYIAVCHPVKALDERTPAKAKLINICIWVLASGVGPIMVMAVTQP 191  
QY 142 MFTSIFTLTMMSVDRYIAVCHPVKALDERTPLKAKIINICIWLLASSVGISALVGGTKV 201  
Db 192 RDGA-VV-CTLQFPSP--SWYWDVTVKICVLFAPVVPILITVCYGLMLRLRSVRLLS 247  
QY 202 REDVDVIECSLQFPDDEYSW-WDLFMKICVEFAFVIPVLIIVCYTLMILRLKSVRLLS 260  
Db 248 GSKEKDRSLRITRMVLVVGAFVVCWAPIHIFIVTWLVDINRRDPLVVAALHLCIALG 307  
QY 261 GSREKDRNLRRITKLVVVAVFIICWTPIHIFILVEALGSTSHSTA-ALSSYFICIALG 319  
Db 308 YANSSSLNPVLYAFLDENFKRCFRQLC 333  
QY 320 YTNSSSLNPVLYAFLDENFKRCFRDFC 345

RESULT 11  
ID US-08-411-859-2 STANDARD; PRI; 372 AA.  
XX xxxxxx  
XX  
DT  
XX Sequence 2, Application US/08411859  
DE

XX Sequence 2, Application US/08411859  
CC Patent No. 5985600  
CC GENERAL INFORMATION:  
CC APPLICANT: EVANS, CHRISTOPHER J.  
CC APPLICANT: KEITH JR., DUANE E.  
CC APPLICANT: EDWARDS, ROBERT H.  
CC TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID  
CC TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED  
CC TITLE OF INVENTION: PHARMACEUTICALS  
CC NUMBER OF SEQUENCES: 15  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Morrison & Foerster  
CC STREET: 755 Page Mill Road  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94304-1018  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/411,859  
CC FILING DATE:  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/929,200  
CC FILING DATE: 13-AUG-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: LITHGOW, TIMOTHY J.  
CC REGISTRATION NUMBER: 36,856  
CC REFERENCE/DOCKET NUMBER: 22000-20526.00  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415-813-5600  
CC TELEFAX: 415-494-0792  
CC TELEX: 706141  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 372 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 372 AA; 40565 MW; 726402 CN;  
  
Query Match 56.3%; Score 1598; DB 2; Length 372;  
Best Local Similarity 66.7%; Pred. No. 2.22e-128;  
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;  
  
Db 47 ALAIAITALYSACVAVGLGNCLVMFGIVRYTKLKTATNIYIFNLALADALATSTLPFQS 106  
QY 57 AIPVITAVYSVVFVGLVGNLSVMFVIIRYTKMKTATNIYIFNLALADALVTTTTPFQS 116  
Db 107 AKYLMETWPFGEILLCKAVLSIDYINMFTSIFTLTMMSVDRYIAVCHPVKALDERTPAKAK 166  
QY 117 AVYLMNSWPFQDVLCKIVISIDYINMFTSIFTLTMMSVDRYIAVCHPVKALDERTPLKAK 176  
Db 167 LINICIWVLASGVGPIMVMAVTQPDGA-VV-CMLQFPSP--SWYWDVTVKICVLFQAF 222  
QY 177 IINICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSW-WDLFMKICVVFQAF 235  
Db 223 VVPIIITVCYGLMLRLRSVRLLSGSKEKDRSLRITRMVLVVGAFVVCWAPIHIFVI 282  
QY 236 VIPVLIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVVVAVFIICWTPIHIFIL 295  
Db 283 VWTLVGINRRDPLVVAALHLCIALGYANSSSLNPVLYAFLDENFKRCFRQLCPTCGRQEP 342  
QY 296 VEALGSTSHSTA-ALSSYFICIALGYTNSSSLNPVLYAFLDENFKRCFRDFCFPIKMRMER 354  
Db 343 GSLRRPRQA 351  
QY 355 QSTNVRVNT 363





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CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/553,058
CC FILING DATE: 11/13/95
CC ATTORNEY/AGENT INFORMATION:
CC NAME: William D. No. 5837809nan, M.D.
CC REGISTRATION NUMBER: 30,878
CC REFERENCE/DOCKET NUMBER: 899-45995/WDN
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (503) 226-7391
CC TELEFAX: (503) 228-9446
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 398 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE:
CC DESCRIPTION: peptide
CC SEQUENCE 398 AA; 44467 MW; 888796 CN;

Query Match 55.4%; Score 1574; DB 2; Length 398;
Best Local Similarity 59.5%; Pred. No. 3.04e-126;
Matches 201; Conservative 60; Mismatches 73; Indels 4; Gaps 4;

Db 46 NRTGLAGNDSLCPQTGSPSMVTAITIMALYSIVCVVGLFGMFLVMYVIVRYTKMKIATNI 105
QY : | | | | | : : : : : | : | | | | | | | | | | | | | | | | | | | |
37 DSNQSVGSEDQQLSESAHISPAIPVITAVYSVVFVVGVLVGNLSVMFEVIRYTKMKIATNI 96

Db 106 YIFNLALADALATSLPFPQSVNYLMGTWPFGTILCKIVISIDYYMMFTSIFTLCMTMSVDR 165
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
97 YIFNLALADALVTTTTPFPQSAVYLMNSWPFGDVLCIKIVISIDYYNMFTSIFTLCMTMSVDR 156

Db 166 YIACHPVKALDERTPRNNAKIVNVCNWILSSAIGLPVMMFMAITKYRQG-S-IDCTLTFSH 223
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
157 YIACHPVKALDERTPPLKAKIINICIWLLASSVGTSAIVLGGTKVREDVDVIECSLQFPD 216

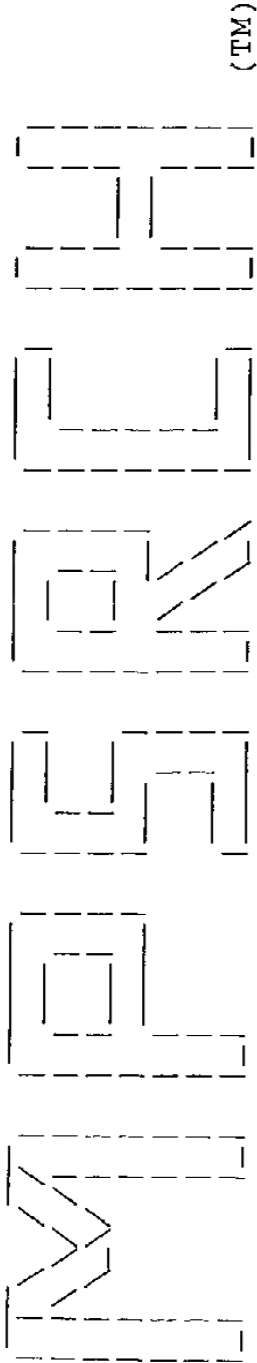
Db 224 PTW-YWENLLKICVFIEAFIMPILIIITVCYGLMILRLKSVRMLSGSKKKDRNLRRITRMV 282
QY | : : | | | | | : : : : : | | | | | | | | | | | | | | | | : : |
217 DEYSWWDLEMKICVFVEAFVIPVLIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLV 276

Db 283 LVVAVTIVCWTPIHIVYIILKALITIPETTFQVSWHFCIALGYTMSCLMPVLYAFLDKM 342
QY | | | | | | | | | | | | | | | | | : : | | | | | | | | | | | |
277 LVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDEN 336

Db 343 TKRCTREFCIPTSSTIEQQNSTVRQNTREHPSTANTV 380
QY | | | | | : | : | : | | | | | | | | | | | | | | | | | | |
337 FKRCFRDFCFPIKMRMERQSTNRVR-NTVQDPASMRDV 373
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Search completed: Thu Feb 17 11:14:36 2000  
Job time : 12 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit.  
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Distribution rights by Oxford Molecular Ltd

Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 17 11:12:22 2000; MasPar time 19.35 Seconds  
Tabular output not generated.  
786.860 Million cell updates/sec

Title: >US-08-455-683-2  
Description: (1-380) from US08455683.pep  
Perfect Score: 2839  
Sequence: 1 MESPIQIFRGDPGPTCPSA.....RNTVQDPASMRDVGGMKRPV 380

Scoring table: PAM 150  
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir60  
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 49.052; Variance 117.295; scale 0.418

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	2839	100.0	380	2	A48227 kappa opioid receptor	0.00e+00
2	2829	99.6	380	2	S36143 kappa opioid receptor	0.00e+00
3	2816	99.2	380	2	JC2434 kappa-opioid receptor	0.00e+00
4	2747	96.8	380	2	JC2338 kappa opioid receptor	0.00e+00
5	2746	96.7	380	2	I57005 opioid receptor kappa	0.00e+00
6	2610	91.9	380	2	A55259 kappa opioid receptor	0.00e+00
7	1687	59.4	373	2	JE0087 delta opioid receptor	0.00e+00
8	1680	59.2	392	2	S65693 opioid receptor mu va	6.02e-263
9	1678	59.1	398	2	A57510 mu opioid receptor -	1.36e-262
10	1677	59.1	400	2	I56553 opiate receptor mu -	2.04e-262
11	1674	59.0	398	2	I56517 mu-opioid receptor -	6.91e-262
12	1659	58.4	398	2	I56504 mu opioid receptor -	3.07e-259
13	1612	56.8	372	2	I38657 delta opiate receptor	6.03e-251
14	1610	56.7	372	2	S34592 delta opioid receptor	1.36e-250
15	1608	56.6	372	2	I38532 delta opioid receptor	3.06e-250
16	1597	56.3	372	2	B48227 delta opioid receptor	2.66e-248
17	1473	51.9	367	2	I56520 G protein-coupled rec	1.83e-226
18	1471	51.8	367	2	JC2421 opioid receptor homol	4.11e-226
19	1470	51.8	367	2	I49022 K3 opiate receptor -	6.16e-226
20	1465	51.6	370	2	S43087 orphan opioid recepto	4.67e-225
21	980	34.5	391	2	C41795 somatostatin receptor	2.26e-140
22	978	34.4	391	2	A39297 somatostatin receptor	5.01e-140
23	976	34.4	391	2	A41795 somatostatin receptor	1.11e-139

24	968	34.1	388	2	JN0605 somatostatin receptor	2.69e-138
25	963	33.9	384	2	A47249 brain-specific somato	1.97e-137
26	954	33.6	384	2	JC4629 somatostatin receptor	7.06e-136
27	936	33.0	369	2	JC2083 somatostatin receptor	9.06e-133
28	927	32.7	369	2	A45291 somatostatin receptor	3.24e-131
29	922	32.5	369	2	D41795 somatostatin receptor	2.36e-130
30	912	32.1	369	2	B41795 somatostatin receptor	1.25e-128
31	909	32.0	346	2	S29248 somatostatin receptor	4.11e-128
32	850	29.9	333	2	I38974 G protein-coupled rec	5.78e-118
33	819	28.8	363	2	I57955 somatostatin receptor	1.20e-112
34	819	28.8	364	2	JN0763 somatostatin receptor	1.20e-112
35	815	28.7	418	2	A46226 somatostatin receptor	5.80e-112
36	792	27.9	328	2	I38973 G protein-coupled rec	5.00e-108
37	788	27.8	363	2	I57940 somatostatin receptor	2.41e-107
38	734	25.9	428	2	S30508 probable G protein-co	3.89e-98
39	732	25.8	428	2	A44021 somatostatin receptor	8.52e-98
40	639	22.5	359	2	S44425 angiotensin II recept	4.72e-82
41	629	22.2	359	2	JC1104 angiotensin II recept	2.27e-80
42	623	21.9	355	2	A45177 chemokine (C-C) recep	2.32e-79
43	617	21.7	359	2	A48857 AT1 angiotensin II re	2.36e-78
44	616	21.7	359	2	S15403 angiotensin II recept	3.48e-78
45	615	21.7	359	2	A42656 angiotensin II recept	5.12e-78

ALIGNMENTS

RESULT 1  
ENTRY A48227 #type complete  
TITLE kappa opioid receptor 1 - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 10-Sep-1997  
ACCESSIONS A48227; JC4138  
REFERENCE A48227  
#authors Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.; Reisine, T.; Bell, G.I.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6736-6740  
#title Cloning and functional comparison of kappa and delta opioid receptors from mouse brain.  
#cross-references MUID:93342064  
#accession A48227  
#status preliminary  
#molecule\_type mRNA  
#residues 1-380 #label YAS  
#cross-references GB:L11065; NID:g348248; PID:g348249  
REFERENCE JC4138  
#authors Liu, H.C.; Lu, S.; Augustin, L.B.; Felsheim, R.F.; Chen, H.C.; Loh, H.H.; Wei, L.N.  
#journal Biochem. Biophys. Res. Commun. (1995) 209:639-647  
#title Cloning and promoter mapping of mouse kappa opioid receptor gene.  
#cross-references MUID:95251663  
#accession JC4138  
#molecule\_type mRNA  
#residues 1-380 #label LIU  
#note The authors translated the codon CAG for residue 365 as Glu

COMMENT This receptor exists in different areas of the central and peripheral nervous systems, and mediates many physiological and pharmacological effects of opiates and opioid compounds.

GENETICS kor  
#gene brain; G protein-coupled receptor; glycoprotein; opioid peptide; phosphoprotein; transmembrane protein  
KEYWORDS #length 380 #molecular-weight 42652 #checksum 9937

SUMMARY  
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Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MESPIQIFRGDPGPTCPSACLLPNSSSWFPNWAESDSNGSVGSEDDQLESAHISPAIPV 60  
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QY 1 MESPIQIFRGDPGPTCPSACLLPNSSSWFPNWAESDSNGSVGSEDDQLESAHISPAIPV 60  
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Db 61 IITAVYSVVFVGLVGNLSLVMEFVIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAVYL 120
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QY 61 IITAVYSVVFVGLVGNLSLVMEFVIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAVYL 120
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Db 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMSVDRYIAVCHPVKALDFRTPLKAKIINI 180
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QY 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMSVDRYIAVCHPVKALDFRTPLKAKIINI 180
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Db 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFVIPVL 240
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QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFVIPVL 240
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Db 241 IIVVCYTLMLRLKSVRLLSGSRKDRNLRRITKLVLVVAVFICWTPIHIFILVEALG 300
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QY 241 IIVVCYTLMLRLKSVRLLSGSRKDRNLRRITKLVLVVAVFICWTPIHIFILVEALG 300
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QY 301 STSHSTAALSSYYFCIALGYTNSSLNPNVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360
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Db 361 RNTVQDPASMRDVGGMNKPV 380
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QY 361 RNTVQDPASMRDVGGMNKPV 380
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RESULT 2
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TITLE kappa opioid receptor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 10-Dec-1993 #sequence_revision 19-Oct-1995 #text_change
29-Jan-1999
ACCESSIONS S36143; S38825; S36102; S39015; A48789
REFERENCE S36143
#authors Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, K.
#journal FEBS Lett. (1993) 330:77-80
#title cDNA cloning and pharmacological characterization of an
opiod receptor with high affinities for
kappa-subtype-selective ligands.
#cross-references MUID:93380575
#accession S36143
#status preliminary
#molecule_type mRNA
#residues 1-380 #label NIS
#cross-references GB:D16534; NID:g409390; PID:d1004487; PID:g415310
S38825
REFERENCE S38825
#authors Chen, Y.; Mestek, A.; Liu, J.; Yu, L.
#journal Biochem. J. (1993) 295:525-528
#title Molecular cloning of a rat kappa opioid receptor reveals
sequence similarities to the mu and delta opioid receptors.
#accession S38825
#status preliminary
#molecule_type mRNA
#residues 1-380 #label CHE
#cross-references GB:L22001; NID:g409236; PID:g409237
S36102
REFERENCE S36102
#authors Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.;
Onogi, T.; Kaneko, S.; Satoh, M.
#journal FEBS Lett. (1993) 329:291-295
#title Cloning and expression of a cDNA for the rat kappa-opioid
receptor.
#cross-references MUID:93374033
#accession S36102
#molecule_type mRNA
#residues 1-41,'L',43-380 #label MIN
#cross-references GB:D16829; NID:g404115; PID:d1004628; PID:g404116
S39015
REFERENCE S39015
#authors Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Deriel, J.K.; Ashby,
B.; Liu-Chen, L.Y.
#journal Biochem. J. (1993) 295:629-633
#title Molecular cloning and expression of a rat kappa opioid
receptor.
#accession S39015
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##molecule_type mRNA
##residues 1-344,'Y',346-380 #label LIS
REFERENCE A48789
#authors Meng, F.; Xie, G.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9954-9958
#title Cloning and pharmacological characterization of a rat kappa
opiod receptor.
#cross-references MUID:94052210
#accession A48789
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-380 #label RES
#cross-references EMBL:U00442; NID:g403486; PID:g403487
KEYWORDS G protein-coupled receptor; transmembrane protein
SUMMARY #length 380 #molecular-weight 42688 #checksum 9972

Query Match 99.6%; Score 2829; DB 2; Length 380;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MESPIQIFRGEPTCPSACLLPNSSSWFPNWAESDSNGSVGSEDQQLSAHISPAIPV 60
|||||
Db 61 IITAVYSVVFVGLVGNLSLVMEFVIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAVYL 120
|||||
QY 61 IITAVYSVVFVGLVGNLSLVMEFVIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAVYL 120
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Db 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMSVDRYIAVCHPVKALDFRTPLKAKIINI 180
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QY 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMSVDRYIAVCHPVKALDFRTPLKAKIINI 180
|||||
Db 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFVIPVL 240
|||||
QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFVIPVL 240
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Db 241 IIVVCYTLMLRLKSVRLLSGSRKDRNLRRITKLVLVVAVFICWTPIHIFILVEALG 300
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QY 241 IIVVCYTLMLRLKSVRLLSGSRKDRNLRRITKLVLVVAVFICWTPIHIFILVEALG 300
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Db 301 STSHSTAALSSYYFCIALGYTNSSLNPNVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360
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QY 301 STSHSTAALSSYYFCIALGYTNSSLNPNVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360
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Db 361 RNTVQDPASMRDVGGMNKPV 380
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QY 361 RNTVQDPASMRDVGGMNKPV 380
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RESULT 3
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TITLE kappa-opioid receptor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change
05-Apr-1995
ACCESSIONS JC2434
REFERENCE JC2434
#authors Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi,
T.
#journal Biochem. Biophys. Res. Commun. (1994) 205:1353-1357
#title Structure and chromosomal mapping of genes for the mouse
kappa-opioid receptor and an opiod receptor homologue
(MOR-C).
#cross-references MUID:95100967
#accession JC2434
#molecule_type mRNA
#residues 1-380 #label NIS
#cross-references DDBJ:D31663
GENETICS
#map_position 1A2-3
#introns 86/2; 204/1
KEYWORDS receptor
SUMMARY #length 380 #molecular-weight 42630 #checksum 9705
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Best Local Similarity 99.5%; Pred. No. 0.00e+00;  
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MESPIQIFRGDPGPTCPSACLLPNSSSWFPNWAESDSNGSVGSEDQQLSAHISPAIPV 60  
Db 61 IITAVYSVVFVVGVLVGNLSLVMFVLIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAVYL 120  
QY 61 IITAVYSVVFVVGVLVGNLSLVMFVLIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAVYL 120  
Db 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180  
QY 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180  
Db 181 CIWLLASSVGISAIVLGGTKVREDVDVIECLLQFPDDEYSWDLFMKICVVFVAFVIPVL 240  
QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECLLQFPDDEYSWDLFMKICVVFVAFVIPVL 240  
Db 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVLVAVVAVFIICWTPIHIFILVEALG 300  
QY 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVLVAVVAVFIICWTPIHIFILVEALG 300  
Db 301 STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360  
QY 301 STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360  
Db 361 RNTVQDPASMRDVGGMNKPV 380  
QY 361 RNTVQDPASMRDVGGMNKPV 380

RESULT 4  
ENTRY JC2338 #type complete  
TITLE kappa opioid receptor - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 10-Sep-1997  
ACCESSIONS JC2338; A55354  
REFERENCE JC2338  
#authors Mansson, E.; Bare, L.; Yang, D.  
#journal Biochem. Biophys. Res. Commun. (1994) 202:1431-1437  
#title Isolation of a human kappa opioid receptor cDNA from placenta.  
#cross-references MUID:94338360  
#accession JC2338  
#molecule\_type mRNA  
#residues 1-380 #label MAN  
#experimental\_source placenta  
REFERENCE A55354  
#authors Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhl, G.R.  
#journal J. Biol. Chem. (1994) 269:25966-25969  
#title Human kappa opiate receptor second extracellular loop elevates dynorphin's affinity for human mu/kappa chimeras.  
#cross-references MUID:95014415  
#accession A55354  
#status preliminary  
#molecule\_type mRNA  
#residues 136-279 #label WAN  
#cross-references GB:L36130; NID:g598184; PID:g598185  
COMMENT This receptor preferentially binds to dynorphins.  
KEYWORDS G protein-coupled receptor; receptor; transmembrane protein  
FEATURE 60-85 #domain transmembrane #status predicted #label TM1\  
95-114 #domain transmembrane #status predicted #label TM2\  
133-154 #domain transmembrane #status predicted #label TM3\  
177-199 #domain transmembrane #status predicted #label TM4\  
228-251 #domain transmembrane #status predicted #label TM5\  
275-296 #domain transmembrane #status predicted #label TM6\  
311-333 #domain transmembrane #status predicted #label TM7  
SUMMARY #length 380 #molecular-weight 42659 #checksum 8304

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Best Local Similarity 93.9%; Pred. No. 0.00e+00;  
Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 1 MESPIQIFRGEPGPTCAPSACLLPNSSAWFPGWAEPDNGSAGSEDAQLEPAHISPAIPV 60  
QY 1 MESPIQIFRGDPGPTCPSACLLPNSSSWFPNWAESDSNGSVGSEDQQLSAHISPAIPV 60  
Db 61 IITAVYSVVFVVGVLVGNLSLVMFVLIIRYTKMKTATNIYIFNLALADALVTTTTPFQSTVYL 120  
QY 61 IITAVYSVVFVVGVLVGNLSLVMFVLIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAVYL 120  
Db 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180  
QY 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180  
Db 181 CIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDDYSWDLFMKICVFIFAFVIPVL 240  
QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWDLFMKICVVFVAFVIPVL 240  
Db 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITRLVLVAVVAVVVCWTPIHIFILVEALG 300  
QY 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVLVAVVAVFIICWTPIHIFILVEALG 300  
Db 301 STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPLKMRMERQSTSRV 360  
QY 301 STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360  
Db 361 RNTVQDPAYLRDIDGMNKPV 380  
QY 361 RNTVQDPASMRDVGGMNKPV 380

RESULT 5  
ENTRY I57005 #type complete  
TITLE opioid receptor kappa-1 - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 29-Aug-1997  
ACCESSIONS I57005  
REFERENCE I57005  
#authors Zhu, J.; Chen, C.; Xue, J.  
#journal Life Sci. (1995) 56:201-207  
#title Cloning of a human .kappa. opioid receptor from the brain.  
#accession I57005  
#status preliminary; translated from GB/EMBL/DBBJ  
#molecule\_type mRNA  
#residues 1-380 #label RES  
#cross-references GB:L37362; NID:g722617; PID:g722618  
GENETICS  
#gene GDB:OPRKL; KOR  
#cross-references GDB:L32651; OMIM:165196  
#map\_position 8q11.2-8q11.2  
SUMMARY #length 380 #molecular-weight 42645 #checksum 8302

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Best Local Similarity 93.7%; Pred. No. 0.00e-00;  
Matches 356; Conservative 18; Mismatches 6; Indels 0; Gaps 0;

Db 1 MDSPIQIFRGEPGPTCAPSACLLPNSSAWFPGWAEPDNGSAGSEDAQLEPAHISPAIPV 60  
QY 1 MESPIQIFRGDPGPTCPSACLLPNSSSWFPNWAESDSNGSVGSEDQQLSAHISPAIPV 60  
Db 61 IITAVYSVVFVVGVLVGNLSLVMFVLIIRYTKMKTATNIYIFNLALADALVTTTTPFQSTVYL 120  
QY 61 IITAVYSVVFVVGVLVGNLSLVMFVLIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAVYL 120  
Db 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180  
QY 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180  
Db 181 CIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDDYSWDLFMKICVFIFAFVIPVL 240







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#authors Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.
#journal Neuron (1993) 11:903-913
#title Cloning and pharmacological characterization of a rat mu
        opioid receptor.
#cross-references MUID:94059560
#accession I58154
#status preliminary; translated from GB/EMBL/DBBJ
#molecule_type mRNA
##residues 1-244,'V',245-398 ##label THO
##cross-references GB:L22455; NID:g437671; PID:g437672
GENETICS
#gene MUOR1
KEYWORDS
SUMMARY
        G protein-coupled receptor; transmembrane protein
        #length 398 #molecular-weight 44508 #checksum 8374
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Best Local Similarity 65.8%; Pred. No. 6.91e-262;
Matches 208; Conservative 54; Mismatches 50; Indels 4; Gaps 4;
Db 68 AITMALYSIVCVVGLFNGFLVMVIVIRYTKMKTATNIYIFNLALADALATSTLPFQSVN 127
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QY 59 PVITAVYSVVFVVGVLVGNLSLVMEVIRYTKMKTATNIYIFNLALADALVTTTMPFQSAV 118
Db 128 YLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVKALDFRTPRNAKIV 187
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 119 YLMNSWPFQDVLCIVISIDYNNMFTSIFTLTMTMSVDRIYAVCHPVKALDFRTPKAKII 178
Db 188 NVCNWILSSAIGLPVMPMATTKYRQG-S-IDCTLTFSSHPTW-YWENLLKICVFIFAFIMP 244
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 179 NICIWLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWDLFMKICVFVFAFVIP 238
Db 245 ILIITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVAVFIVCVIPIHIYVLIKA 304
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 239 VLIITVCYTLMIILRLKSVRLSGSREKDRNLRRITKLVLVVAVFIICTWPIHIFILVEA 298
Db 305 LITIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFRFCIPTSSSTIEQNSI 364
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 299 LGSISHSTAALSSYYFCIALGYTNSCLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTN 358
Db 365 RVRQNTREHPSTANTV 380
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QY 359 RVR-NTVQDPASMRDV 373
RESULT 12
ENTRY I56504 #type complete
TITLE mu opioid receptor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
        26-Jul-1996
ACCESSIONS I56504
REFERENCE I56504
#authors Zastawny, R.L.; George, S.R.; Nguyen, T.; Cheng, R.; Tsatsos,
        J.; Briones-Urbina, R.; O'Dowd, B.F.
#journal J. Neurochem. (1994) 62:2099-2105
#title Cloning, characterization, and distribution of a mu-opioid
        receptor in rat brain.
#cross-references MUID:94246380
#accession I56504
#status preliminary; translated from GB/EMBL/DBBJ
#molecule_type mRNA
##residues 1-398 ##label RES
##cross-references EMBL:U35424; NID:g1017731; PID:g1017732
SUMMARY
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Matches 208; Conservative 53; Mismatches 51; Indels 4; Gaps 4;
Db 68 AITMALYSIVCVVGLFNGFLVMVIVIRYTKMKTATNIYIFNLALADALATSTLPFQSVN 127
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 59 PVITAVYSVVFVVGVLVGNLSLVMEVIRYTKMKTATNIYIFNLALADALVTTTMPFQSAV 118
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Db 128 YLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVKALDFRTPRNAKIV 187
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QY 119 YLMNSWPFQDVLCIVISIDYNNMFTSIFTLTMTMSVDRIYAVCHPVKALDFRTPKAKII 178
Db 188 NVCNWILSSAIGLPVMPMATTKYRQG-S-IDCTLTFSSHPTW-YWENLLKICVFIFAFIMP 244
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 179 NICIWLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWDLFMKICVFVFAFVIP 238
Db 245 VLIITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVAVFIVCVIPIHIYVLIKA 304
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QY 239 VLIITVCYTLMIILRLKSVRLSGSREKDRNLRRITKLVLVVAVFIICTWPIHIFILVEA 298
Db 305 LITIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFRFCIPTSSSTIEQNSI 364
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QY 299 LGSISHSTAALSSYYFCIALGYTNSCLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTN 358
Db 365 RVRQNTREHPSTANTV 380
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QY 359 RVR-NTVQDPASMRDV 373
RESULT 13
ENTRY I38657 #type complete
TITLE delta opiate receptor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
        06-Sep-1996
ACCESSIONS I38657
REFERENCE I38657
#authors Simonin, F.; Befort, K.; Gaveriaux-Ruff, C.; Matthes, H.;
        Nappey, V.; Lannes, B.; Micheleletti, G.; Kieffer, B.
#journal Mol. Pharmacol. (1994) 46:1015-1021
#title The human delta-opioid receptor: genomic organization, cDNA
        cloning, functional expression, and distribution in human
        brain.
#cross-references MUID:95107267
#accession I38657
#status preliminary; translated from GB/EMBL/DBBJ
#molecule_type mRNA
##residues 1-372 ##label RES
##cross-references EMBL:U10504; NID:g501144; PID:g501145
SUMMARY
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Best Local Similarity 63.1%; Pred. No. 6.03e-251;
Matches 217; Conservative 60; Mismatches 58; Indels 9; Gaps 8;
Db 15 LFANASDAYPS-A-CPSAGANASGPPGARSAS-SIALAIAITAIYASVAVGLLGNVLVM 71
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 22 LLPNSSWFPNWAESDNGSVGSEDQQLSEAHISPAIPVIITAVYSVVFVVGVLVGNSLVM 81
Db 72 FGIVRYTKMKTATNIYIFNLALADALATSTLPFQSAKYLMETWPFGEILLCKAVLSIDYIN 131
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 82 FVIIRYTKMKTATNIYIFNLALADALVTTTTPQSAVYLMNSWPFQDVLCIVISIDYIN 141
Db 132 MFTSIFTLTMTMSVDRIYAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIVMVAVTRP 191
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 142 MFTSIFTLTMTMSVDRIYAVCHPVKALDFRTPKAKIINICIWLLASSVGISAIVLGGTKV 201
Db 192 RDGA-VV-CMLQFPSP--SWYWDVTVKICVFLEAFVVPVPIIITVCYGLMLRLSVRLLS 247
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 202 REDVDVIECSLQFPDDDEYSW-WDLFMKICVFVFAFVIPVLIIVCYTTLRLKSVRLLS 260
Db 248 GSKEKDRSLRRITRMVLVVVGAFFVVCWAPIHIIVVWTLVDIDRRDPLVVVAALHLCIALG 307
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QY 261 GSREKDRNLRRITKLVLVVAVFIICTWPIHIFILVEALGSTSHSTA-ALSSYFICIALG 319
Db 308 YANSSNLNPVLYAFLDENFKRCFRQLCRKPCGRDPDPSFSRAREA 351
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 320 YTNSSNLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNVRNT 363
RESULT 14
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ENTRY          S34592      #type complete
TITLE          delta opioid receptor - rat
ORGANISM       #formal_name Rattus norvegicus #common_name Norway rat
DATE           10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
                29-Jan-1999
ACCESSIONS     S34592; I56571
REFERENCE      Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
                FEBS Lett. (1993) 327:311-314
                Primary structures and expression from cDNAs of rat opioid
                receptor delta- and mu-subtypes.
#cross-references MUID:93351652
#accession      S34592
##molecule_type mRNA
##residues      1-372 #label FUK
##cross-references GB:D16348; NID:g391864; PID:d1004367; PID:g391865
REFERENCE      I56571
                Abood, M.E.
                J. Neurosci. Res. (1994) 27:714-719
                Molecular cloning and expression of a rat delta opioid
                receptor from rat brain.
#accession      I56571
##status        preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues      1-372 #label RES
##cross-references EMBL:U00475; NID:g403488; PID:g514211
GENETICS       dorl
#gene           G protein-coupled receptor; transmembrane protein
KEYWORDS       #length 372 #molecular-weight 40449 #checksum 2221
SUMMARY        Query Match          56.7%; Score 1610; DB 2; Length 372;
                Best Local Similarity 65.6%; Pred. No. 1.36e-250;
                Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;

Db 15 LLANVSDTFPSAFPASANASGSPGAR--SAS-SLALATAITALYSACVAVGLGNVLVM 71
QY 22 LLPNSSWFFPNWAESDSNGSVGSEDQQLSAHISPAIPVIITAVYSVVFVGLVGNLVM 81
Db 72 FGIVRYTKLKTATNIYIFNLALADALATSTLPFQSAKYLMETWPFGEGLCKAVLSIDYIN 131
QY 82 FVIIRYTKMTATNIYIFNLALADALVTTTMTFQSAVYLMNSWPFQGVLCIVISIDYIN 141
Db 132 MFTSIFTLTMSVDRIYAVCHPVKALDERTPAKAKLINICIWVLASGVGVPIMVAVTQP 191
QY 142 MFTSIFTLTMSVDRIYAVCHPVKALDERTPLKAKLINICIWLLASSVGISAVLGGTKV 201
Db 192 RDGA-VV-CILQFPSP--SWYWDVTVKICVLEAFVVPILIIIVCYGLMLRLRSVRLLS 247
QY 202 REDVDVIECSLQFPDDEYSW-WDLFMKICVVFVAFVIPVLIIVCYTLMILRLKSVRLLS 260
Db 248 GSKEKDRSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALG 307
QY 261 GSREKDRNLRRITKLVVVAVVFIICWTPIHIFILVEALGSTSHSTA-ALSSYVFCIALG 319

Db 308 YANSSLPVLYAFLDENFKRCFRQLC 333
QY 320 YTNSSLPVLYAFLDENFKRCFRDFC 345

RESULT 15
ENTRY          I38532      #type complete
TITLE          delta opioid receptor - human
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           29-May-1998 #sequence_revision 29-May-1998 #text_change
                29-May-1998
ACCESSIONS     I38532
REFERENCE      Knapp, R.J.; Malatynska, E.; Fang, L.; Xiaoping, L.; Nguyen,
                M.; Santoro, G.; Varga, E.V.; Hruby, V.J.; Roeske, W.R.;
                Yamamura, H.I.
                Life Sci. (1994) 54:PL463-PL469
                Identification of a human delta opioid receptor: Cloning and
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expression.
#cross-references MUID:94260835
#accession      I38532
##status        preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues      1-372 #label RES
##cross-references EMBL:U07882; NID:g497313; PID:g497314
SUMMARY        #length 372 #molecular-weight 40450 #checksum 2484

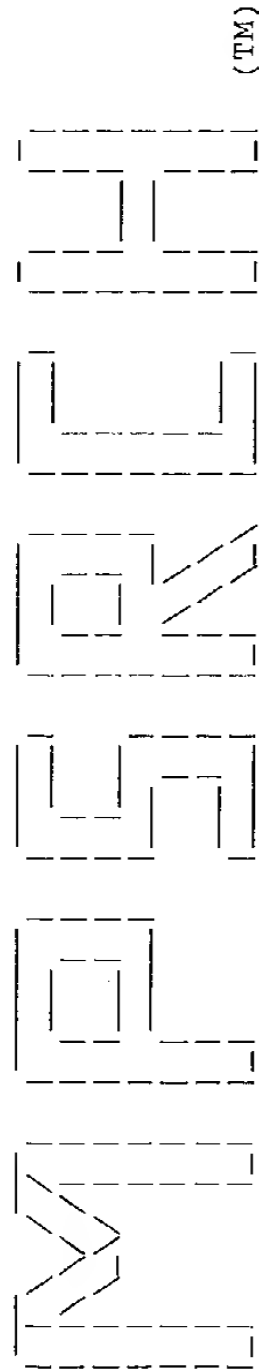
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                Best Local Similarity 65.3%; Pred. No. 3.06e-250;
                Matches 213; Conservative 56; Mismatches 48; Indels 9; Gaps 8;

Db 15 LFANASDAYPS-A-FPSAGANASGPPGPGSAS-SLALATAITALYSACVAVGLGNVLVM 71
QY 22 LLPNSSWFFPNWAESDSNGSVGSEDQQLSAHISPAIPVIITAVYSVVFVGLVGNLVM 81
Db 72 FGIVRYTKMTATNIYIFNLALADALATSTLPFQSAKYLMETWPFGEGLCKAVLSIDYIN 131
QY 82 FVIIRYTKMTATNIYIFNLALADALVTTTMTFQSAVYLMNSWPFQGVLCIVISIDYIN 141
Db 132 MFTSIFTLTMSVDRIYAVCHPVKALDERTPAKAKLINICIWVLASGVGVPIMVAVTRP 191
QY 142 MFTSIFTLTMSVDRIYAVCHPVKALDERTPLKAKLINICIWLLASSVGISAVLGGTKV 201
Db 192 RDGA-VV-CMLQFPSP--SWYWDVTVKICVLELFAFVVPILIIIVCYGLMLRLRSVRLLS 247
QY 202 REDVDVIECSLQFPDDEYSW-WDLFMKICVVFVAFVIPVLIIVCYTLMILRLKSVRLLS 260
Db 248 GSKEKDRSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDIDRRDPLVVAALHLCIALG 307
QY 261 GSREKDRNLRRITKLVVVAVVFIICWTPIHIFILVEALGSTSHSTA-ALSSYVFCIALG 319

Db 308 YANSSLPVLYAFLDENFKRCFRQLC 333
QY 320 YTNSSLPVLYAFLDENFKRCFRDFC 345

Search completed: Thu Feb 17 11:12:44 2000
Job time : 22 secs.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 17 11:13:01 2000; MasPar time 13.32 Seconds  
Tabular output not generated. 806.224 Million cell updates/sec

Title: >US-08-455-683-2  
Description: (1-380) from US08455683.pap  
Perfect Score: 2839  
Sequence: 1 MESPIQIFRGDPGPTCPSA.....RNTVQDPASMRDVGGMNKPV 380

Scoring table: PAM 150  
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot37  
1:swissprot

Statistics: Mean 50.173; Variance 102.089; scale 0.491

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	2839	100.0	380	1	OPRK_MOUSE	KAPPA-TYPE OPIOID RECE	0.00e+00
2	2829	99.6	380	1	OPRK_RAT	KAPPA-TYPE OPIOID RECE	0.00e+00
3	2747	96.8	380	1	OPRK_HUMAN	KAPPA-TYPE OPIOID RECE	0.00e+00
4	2610	91.9	380	1	OPRK_CAVPO	KAPPA-TYPE OPIOID RECE	0.00e+00
5	1678	59.1	398	1	OPRM_MOUSE	MU-TYPE OPIOID RECEPTO	0.00e+00
6	1677	59.1	400	1	OPRM_HUMAN	MU-TYPE OPIOID RECEPTO	0.00e+00
7	1676	59.0	398	1	OPRM_RAT	MU-TYPE OPIOID RECEPTO	0.00e+00
8	1672	58.9	401	1	OPRM_PIG	MU-TYPE OPIOID RECEPTO	0.00e+00
9	1650	58.1	401	1	OPRM_BOVIN	MU-TYPE OPIOID RECEPTO	1.71e-302
10	1612	56.8	372	1	OPRD_HUMAN	DELTA-TYPE OPIOID RECE	1.27e-294
11	1510	56.7	372	1	OPRD_RAT	DELTA-TYPE OPIOID RECE	3.30e-294
12	1597	56.3	372	1	OPRD_MOUSE	DELTA-TYPE OPIOID RECE	1.52e-291
13	1473	51.9	367	1	OPRX_RAI	NOCICEPTIN RECEPTOR (O	7.03e-266
14	1471	51.8	367	1	OPRX_MOUSE	NOCICEPTIN RECEPTOR (O	1.82e-265
15	1465	51.6	370	1	OPRX_HUMAN	NOCICEPTIN RECEPTOR (O	3.15e-264
16	1459	51.4	370	1	OPRX_PIG	NOCICEPTIN RECEPTOR (O	5.46e-263
17	1447	51.0	370	1	OPRX_CAVPO	NOCICEPTIN RECEPTOR (O	1.64e-260
18	1273	44.8	228	1	OPRD_PIG	DELTA-TYPE OPIOID RECE	1.09e-224
19	980	34.5	391	1	SSR1_MOUSE	SOMATOSTATIN RECEPTOR	7.81e-165
20	978	34.4	391	1	SSR1_RAT	SOMATOSTATIN RECEPTOR	1.99e-164
21	976	34.4	391	1	SSR1_HUMAN	SOMATOSTATIN RECEPTOR	5.06e-164
22	968	34.1	388	1	SSR4_HUMAN	SOMATOSTATIN RECEPTOR	2.13e-162
23	963	33.9	384	1	SSR4_RAT	SOMATOSTATIN RECEPTOR	2.20e-161

24	954	33.6	384	1	SSR4_MOUSE	SOMATOSTATIN RECEPTOR	1.47e-159
25	938	33.0	368	1	SSR2_BOVIN	SOMATOSTATIN RECEPTOR	2.56e-156
26	936	33.0	369	1	SSR2_PIG	SOMATOSTATIN RECEPTOR	6.50e-156
27	927	32.7	369	1	SSR2_RAT	SOMATOSTATIN RECEPTOR	4.32e-154
28	922	32.5	369	1	SSR2_MOUSE	SOMATOSTATIN RECEPTOR	4.43e-153
29	912	32.1	369	1	SSR2_HUMAN	SOMATOSTATIN RECEPTOR	4.67e-151
30	850	29.9	333	1	GPR8_HUMAN	PROBABLE G PROTEIN-COU	1.52e-138
31	819	28.8	362	1	SSR5_MOUSE	SOMATOSTATIN RECEPTOR	2.61e-132
32	819	28.8	363	1	SSR5_HUMAN	SOMATOSTATIN RECEPTOR	2.61e-132
33	815	28.7	418	1	SSR3_HUMAN	SOMATOSTATIN RECEPTOR	1.66e-131
34	792	27.9	328	1	GPR7_HUMAN	PROBABLE G PROTEIN-COU	6.86e-127
35	788	27.8	363	1	SSR5_RAT	SOMATOSTATIN RECEPTOR	4.35e-126
36	734	25.9	428	1	SSR3_RAI	SOMATOSTATIN RECEPTOR	2.73e-115
37	732	25.8	428	1	SSR3_MOUSE	SOMATOSTATIN RECEPTOR	6.85e-115
38	639	22.5	359	1	AG2R_CANFA	TYPE-1 ANGIOTENSIN II	1.97e-96
39	635	22.4	98	1	OPRM_CAVPO	MU-TYPE OPIOID RECEPTO	1.21e-95
40	629	22.2	359	1	AG2R_HUMAN	TYPE-1A ANGIOTENSIN II	1.85e-94
41	626	22.1	359	1	AG2R_PIG	TYPE-1 ANGIOTENSIN II	7.21e-94
42	623	21.9	355	1	CKR1_HUMAN	C-C CHEMOKINE RECEPTOR	2.81e-93
43	617	21.7	359	1	AG2R_RABIT	TYPE-1 ANGIOTENSIN II	4.27e-92
44	616	21.7	359	1	AG2R_BOVIN	TYPE-1 ANGIOTENSIN II	6.72e-92
45	615	21.7	372	1	GALS_RAT	GALANIN RECEPTOR TYPE	1.06e-91

ALIGNMENTS

RESULT 1  
ID OPRK\_MOUSE STANDARD; PRT; 380 AA.  
AC P33534;  
DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).  
GN OPRK1.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 93342064.  
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,  
RA BELL G.I.;  
RT "Cloning and functional comparison of kappa and delta opioid  
RT receptors from mouse brain."  
RL PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95100967.  
RA NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;  
RT "Structure and chromosomal mapping of genes for the mouse  
RT kappa-opioid receptor and an opioid receptor homologue (MOR-C).";  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95251663.  
RA LIU H.C., LU S., AUGUSTIN L.B., FELSHEIM R.F., CHEN H.C.,  
RA LOH H.H., WEI L.N.;  
RT "Cloning and promoter mapping of mouse kappa opioid receptor gene."  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 209:639-647(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 96084989.  
RA BELKOWSKI S.M., ZHU J., LIU-CHEN L.Y., EISENSTEIN T.K.,  
RA ADLER M.W., ROGERS T.J.;  
RT "Sequence of kappa-opioid receptor cDNA in the R1.1 thymoma cell  
RT line."  
RL J. NEUROIMMUNOL. 62:113-117(1995).  
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
CC FOR DOPAMINE. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.



CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
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CC -----  
CC EMBL; L22001; G409237; -.  
CC EMBL; D16829; G404116; -.  
CC EMBL; L22536; G425189; -.  
CC EMBL; U00442; G403487; -.  
CC EMBL; D16534; G415310; -.  
CC EMBL; U17995; G727260; -.  
CC EMBL; U17993; G727260; JOINED.  
CC EMBL; U17994; G727260; JOINED.  
CC PIR; S36143; S36143.  
CC PIR; S38825; S38825.  
CC GCRDB; GCR\_0636; -.  
CC GCRDB; GCR\_0724; -.  
CC GCRDB; GCR\_0790; -.  
CC GCRDB; GCR\_0804; -.  
CC GCRDB; GCR\_1282; -.  
CC PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.  
CC PFAM; PF00001; 7tm\_1; 1.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 174 196 4 (POTENTIAL).  
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOHYD 25 25 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
FT CONFLICT 42 42 V -> L (IN REF. 2).  
FT CONFLICT 345 345 C -> Y (IN REF. 3).  
SQ SEQUENCE 380 AA; 42688 MW; EE858A46 CRC32;

Query Match 99.6%; Score 2829; DB 1; Length 380;  
Best Local Similarity 98.9%; Pred. No. 0.00e+00;  
Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 MESPIQIFRGEPTCAPSACLLPNSSWFPNWAESDNGSVGSEDQQLPAHISAIPV 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 1 MESPIQIFRGDPGTCPSACLLPNSSWFPNWAESDNGSVGSEDQQLSAHISAIPV 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 IITAVYSWVFGVGLVGNLSVMFVIIRYTKMTATNIYIFNLALADALVTTTMPFQSAVYL 120  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 IITAVYSWVFGVGLVGNLSVMFVIIRYTKMTATNIYIFNLALADALVTTTMPFQSAVYL 120  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 121 MNSWPFQDVLCKIVISIDYNNMTSIFTLIMMSVDRIYAVCHPVKALDFRTPLKAKIINI 180  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 121 MNSWPFQDVLCKIVISIDYNNMTSIFTLIMMSVDRIYAVCHPVKALDFRTPLKAKIINI 180  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWDLFMKICVFAFVPIVL 240  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWDLFMKICVFAFVPIVL 240  
Db 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVVVVAVFIICWTPIHIFILVEALG 300  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVVVVAVFIICWTPIHIFILVEALG 300  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 301 STSHSTAVLSSYFICIALGYTNSSLNPVLYAFLDENFKRFRDFCFPIKMRMERQSTNRV 360  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 301 STSHSTAALSSYFICIALGYTNSSLNPVLYAFLDENFKRFRDFCFPIKMRMERQSTNRV 360  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 361 RNTVQDPASMRDVGGMNKPV 380  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 361 RNTVQDPASMRDVGGMNKPV 380  
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RESULT 3  
ID OPRK\_HUMAN STANDARD; PRT; 380 AA.  
AC P41145;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).  
GN OPRK1 OR OPRK.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RX MEDLINE; 94338360.  
RA MANSSON E., BARE L.A., YANG D.;  
RT "Isolation of a human kappa opioid receptor cDNA from placenta.";  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RX MEDLINE; 95350200.  
RA SIMONIN F., GAVERIAUS-RUFF C., BEFORT K., LANNES B., MICHELETTI G.,  
RT "Kappa-Opioid receptor in humans: cDNA and genomic cloning,  
RT chromosomal assignment, functional expression, pharmacology, and  
RT expression pattern in the central nervous system.";  
RL PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 95174504.  
RA ZHU J., CHEN C., XUE J.-C., KUNAPULI S., DERIEL J.K., LIU-CHEN L.-Y.;  
RT "Cloning of a human kappa opioid receptor from the brain.";  
RL LIFE SCI. 56:201-207(1995).  
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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CC -----  
CC EMBL; U11053; G532060; -.  
CC EMBL; U17298; G596070; -.  
CC EMBL; L37362; G722618; -.  
CC PIR; JC2338; JC2338.  
CC GCRDB; GCR\_1819; -.  
CC GCRDB; GCR\_2026; -.  
CC GCRDB; GCR\_2054; -.  
CC MIM; 165196; -.

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DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 EXTRACELLULAR (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
FT CONFLICT 2 2 E -> D (IN REF. 2 AND 3).
SQ SEQUENCE 380 AA; 42659 MW; 1980629E CRC32;

Query Match 96.8%; Score 2747; DB 1; Length 380;
Best Local Similarity 93.9%; Pred. No. 0.00e+00;
Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 1 MESPIQIFRGEPTCAPSACLPNSSAWFPGWAEPDNGSAGSEDAQLEPAHISPAIPV 60
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QY 1 MESPIQIFRGDPGFCSPSACLLPNSSWFFNWAESDSNGSVGSEDOQLESAHISPAIPV 60
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 IITAVYSVVFVGLVGNLSVMFVIIRYTKMKTATNIYIFNLALADALVTTMPFQSTVYL 120
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 IITAVYSVVFVGLVGNLSVMFVIIRYTKMKTATNIYIFNLALADALVTTMPFQSAVYL 120
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMMNSVDRIYIACHVPVKALDERTPLKAKIINI 180
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 MNSWPFQDVLCKIVISIDYNNMFTSIFTLTMMNSVDRIYIACHVPVKALDERTPLKAKIINI 180
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 181 CIWLLSSVGISAIVLGGTKVREDVDVIECSLQFPDDDDYSWWDLFMKICVFIFAVIPVL 240
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWWDLFMKICVFVFAFVIPVL 240
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 241 IIVCYTLMILRLKSVRLLSGSRKDRNLRRITRLVLVAVFVVCWTPFIHIFILVEALG 300
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 241 IIVCYTLMILRLKSVRLLSGSRKDRNLRRITKLVLVVAVFIICTWTPFIHIFILVEALG 300
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Db 301 STSHSTAALSSYYFCIALGYTNSSLNPILYAFLDENFKRCFRDFCFPLKMRMERQSTSRV 360
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QY 301 STSHSTAALSSYYFCIALGYTNSSLPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 361 RNTVQDPAYLRDIDGMKNKPV 380
   |||||:||||:||||:
QY 361 RNTVQDPASMRDVGGMKNKPV 380
   |||||:||||:||||:

RESULT 4
ID OPRK_CAVPO STANDARD; PRT; 380 AA.
AC P41144;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN OPRK1.
OS CAVIA PORCELLUS (GUINEA PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY; TISSUE=BRAIN;
```

```
RX MEDLINE; 94224825.
RA XIE G.X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,
RA GOLDSTEIN A., WATSON S.J., AKIL H.;
RT "Primary structure and functional expression of a guinea pig kappa
RT opioid (dynorphin) receptor.";
RL PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).
CC -|- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; U04092; G476107; -.
DR GCRDB; GCR_0991; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 BY SIMILARITY.
FT DISULFID 131 210 PALMITATE (POTENTIAL).
FT LIPID 345 345 POTENTIAL.
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
SQ SEQUENCE 380 AA; 42736 MW; F9F34C4C CRC32;

Query Match 91.9%; Score 2610; DB 1; Length 380;
Best Local Similarity 92.9%; Pred. No. 0.00e+00;
Matches 338; Conservative 21; Mismatches 5; Indels 0; Gaps 0;

Db 17 ARNACLLPNSGSAWLPGWAEPDNGSAGPQDQLEPAHISPAIPVIITAVYSWVFGVLVG 76
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QY 17 SPSACLLPNSSSWFFNWAESDSNGSVGSEDOQLESAHISPAIPVIITAVYSWVFGVLVG 76
   : :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 77 NSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMTPEQSTVYLMNSWPFQDVLCKIVIS 136
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QY 77 NSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMTPEQSAVYLMNSWPFQDVLCKIVIS 136
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Db 137 IDYNNMFTSIFTLTMMNSVDRIYIACHVPVKALDERTPLKAKIINICIWLLSSSVGISAAIL 196
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QY 137 IDYNNMFTSIFTLTMMNSVDRIYIACHVPVKALDERTPLKAKIINICIWLLASSVGISAIVL 196
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 197 GGTKVREDVDVIECSLQFPDDDDYSWWDLFMKICVFVFAFVIPVLIIIVCYTLMILRLKSV 256
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 197 GGTKVREDVDVIECSLQFPDDDEYSWWDLFMKICVFVFAFVIPVLIIIVCYTLMILRLKSV 256
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 257 RLLSGSREKDRNLRRITRLVLVAVFVVCWTPFIHIFILVEALGSTSHSTAALSSYYFCI 316
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 257 RLLSGSREKDRNLRRITKLVLVVAVFIICTWTPFIHIFILVEALGSTSHSTAALSSYYFCI 316
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 317 ALGYTNSSLNPILYAFLDENFKRCFRDFCFPIKMRMERQSTSRVNTVQDPAYMRNVGDV 376
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RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RA MESTEK A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M.,  
RA CHEN Y., YU L.;  
RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
[3]  
RN SEQUENCE FROM N.A.  
RP  
RC TISSUE=BRAIN;  
RX MEDLINE; 95046336.  
RA BARE L.A., MANSSON E., YANG D.;  
RT "Expression of two variants of the human mu opioid receptor mRNA in  
RT SK-N-SH cells and human brain.";  
RL FEBS LETT. 354:213-216(1994).  
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
CC FOR BETA-ENDORPHIN.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
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CC -----  
DR EMBL; L25119; G452073; -.  
DR EMBL; L29301; G459832; -.  
DR EMBL; U12569; G607912; -.  
DR GCRDB; GCR\_0885; -.  
DR GCRDB; GCR\_0966; -.  
DR GCRDB; GCR\_2042; -.  
DR MIM; 600018; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.  
DR PFAM; PF00001; 7tm\_1; 1.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE; ALTERNATIVE SPLICING.  
FT DOMAIN 1 66  
FT TRANSMEM 67 96  
FT DOMAIN 97 105  
FT TRANSMEM 106 123  
FT DOMAIN 124 145  
FT TRANSMEM 146 165  
FT DOMAIN 166 195  
FT TRANSMEM 196 211  
FT DOMAIN 212 236  
FT TRANSMEM 237 259  
FT DOMAIN 260 282  
FT TRANSMEM 283 305  
FT DOMAIN 306 313  
FT TRANSMEM 314 330  
FT DOMAIN 331 400  
FT DISULFID 142 219  
FT LIPID 353 353  
FT CARBOHYD 9 9  
FT CARBOHYD 12 12  
FT CARBOHYD 33 33  
FT CARBOHYD 40 40  
FT CARBOHYD 48 48  
FT VARSPLIC 389 400  
FT CONFLICT 40 40  
FT CONFLICT 51 51  
FT CONFLICT 207 207  
FT CONFLICT 234 234  
SQ SEQUENCE 400 AA; 44779 MW; 1AFC0337 CRC32;  
  
Query Match 59.1%; Score 1677; DB 1; Length 400;  
Best Local Similarity 66.6%; Pred. No. 0.00e-00;  
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;  
  
Db 70 AITMALYSIVCVGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLFPQSVN 129

QY 59 PVIITAVYSVVFVVGVLGNSLVMEVIRYTKMKTATNIYIFNLALADALVTTMPFQSAV 118  
Db 130 YLMGTWPEFTILCKIVISIDYNNMFTSIPTLCTMSVDRIYAVCHPVKALDERTPRNAKII 189  
QY 119 YLMNSWPEFGDLCKIVISIDYNNMFTSIPTLCTMSVDRIYAVCHPVKALDERTPLKAKII 178  
Db 190 NVCNWILSSAIGLPVMMATTKYRQG-S-IDCTLTFESHPTW-YWENLLKICVFIFAFIMP 246  
QY 179 NICIWLASSVGISAIVLGGTKVREDVDIECSLQFPDDDEYSWDLFMKICVFVFAFVIP 238  
Db 247 VLIITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVAVFVVCWTPHIHYVVIKA 306  
QY 239 VLIITVCYILMILRLKSVRLSGSREKDRNLRRITKLVLVVAVFVVCWTPHIHFILVEA 298  
Db 307 LVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFRFCIPTSSNIEQQNST 366  
QY 299 LGSTSHSTAALSSYFICIALGYTNSCLNPVLYAFLDENFKRCFRFCIPKMRMERQSTN 358  
Db 367 RIRQNTRDHPS 377  
QY 359 RVRNTVQDPAS 369  
  
RESULT 7  
ID OPRM\_RAT STANDARD; PRT; 398 AA.  
AC P33535; Q64064; Q62846; Q64120;  
DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
DE MU-TYPE OPIOID RECEPTOR (MOR-1) (OPIOID RECEPTOR B) (MUOR1).  
GN OPRM1 OR MOR-B.  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 93351652.  
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;  
RT "Primary structures and expression from cDNAs of rat opioid receptor  
RT delta- and mu-subtypes.";  
RL FEBS LETT. 327:311-314(1993).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 94052137.  
RA WANG J.-B., IMAI Y., EPLER M.C., GREGOR P., SPIVAK C., UHL G.R.;  
RT "Mu opiate receptor: cDNA cloning and expression.";  
RL PROC. NATL. ACAD. SCI. U.S.A. 90:10230-10234(1993).  
[3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 93341493.  
RA CHEN Y., MESTEK A., LIU J., HURLEY J.A., YU L.;  
RT "Molecular cloning and functional expression of a mu-opioid receptor  
RT from rat brain.";  
RL MOL. PHARMACOL. 44:8-12(1993).  
[4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RA BUNZOW J.R., GRANDY D.K., KELLY M.;  
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.  
[5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=OLFACTORY BULB;  
RX MEDLINE; 94059560.  
RA THOMPSON R.C., MANSOUR A., AKIL H., WATSON S.J.;  
RT "Cloning and pharmacological characterization of a rat mu opioid  
RL NEURON 11:903-913(1993).  
[6]  
RP SEQUENCE FROM N.A.



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CC -----
DR EMBL; L38645; G1553057; -.
DR GCRDB; GCR_1287; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 67 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 68 97 1 (POTENTIAL).
FT DOMAIN 98 106 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 107 124 2 (POTENTIAL).
FT DOMAIN 125 146 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 147 166 3 (POTENTIAL).
FT DOMAIN 167 196 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 197 212 4 (POTENTIAL).
FT DOMAIN 213 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 260 5 (POTENTIAL).
FT DOMAIN 261 283 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 284 306 6 (POTENTIAL).
FT DOMAIN 307 314 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 315 331 7 (POTENTIAL).
FT DOMAIN 332 401 CYTOPLASMIC (POTENTIAL).
FT DISULFID 143 220 BY SIMILARITY.
FT LIPID 354 354 PALMITATE (POTENTIAL).
FT CARBOHYD 9 9 POTENTIAL.
FT CARBOHYD 12 12 POTENTIAL.
FT CARBOHYD 34 34 POTENTIAL.
FT CARBOHYD 41 41 POTENTIAL.
FT CARBOHYD 49 49 POTENTIAL.
SQ SEQUENCE 401 AA; 45098 MW; 6786FD94 CRC32;
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Query Match 58.9%; Score 1672; DB 1; Length 401;  
Best Local Similarity 66.6%; Pred. No. 0.00e+00;  
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

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Db 71 AITIMALYSIVCVVGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVN 130
QY 59 PVIITAVYSVVFVGLVGNLSLVMFVIRYTKMKTATNIYIFNLALADALVTTMPFQSAV 118

Db 131 YLMGTWPFGTILCKIVISIDYNNMFTSIETLCTMSVDRIYAVCHPVKALDFTPRNAKII 190
QY 119 YLMNSWPFQDVLCIKIVISIDYNNMFTSIETLTMMMSVDRIYAVCHPVKALDFTPLKAKII 178

Db 191 NVCNWILSSAIGLPVFMFMATTKYRNG-S-IDCALTFESHPTW-YWENLLKICVFIFAFIMP 247
QY 179 NICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWWDLEFMKICVFVFAFVIP 238

Db 248 VLIITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVAVFVVCWTPPIHIYVIAKA 307
QY 239 VLIITVCYTLMLRLKSVRLLSGSREKDRNLRRITKLVLVVAVFIICWTPPIHIFILVEA 298

Db 308 LITIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFRFCPTSTTIEQQNSA 367
QY 299 LGSTSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFFCIKMRMERQSTN 358

Db 368 RIRQNTDRHPS 378
QY 359 RVRNTVQDPAS 369
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RESULT 9  
ID OPRM\_BOVIN STANDARD; PRT; 401 AA.  
AC P79350;  
DT 15-JUL-1998 (REL. 36, CREATED)  
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
DE MU-TYPE OPIOID RECEPTOR (MOR-1).  
GN OPRM1.  
OS BOS TAURUS (BOVINE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOS.  
RN [1]  
RP SEQUENCE FROM N.A.

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RC TISSUE=STRIATUM;
RA SIMON E.J., VILLEM S., ANDRIA M., ONOPRISHVILI I., HILLER J.M.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDORPHIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; U89677; G1881731; -.
DR GCRDB; GCR_1213; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 67 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 68 97 1 (POTENTIAL).
FT DOMAIN 98 106 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 107 124 2 (POTENTIAL).
FT DOMAIN 125 146 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 147 166 3 (POTENTIAL).
FT DOMAIN 167 196 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 197 212 4 (POTENTIAL).
FT DOMAIN 213 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 260 5 (POTENTIAL).
FT DOMAIN 261 283 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 284 306 6 (POTENTIAL).
FT DOMAIN 307 314 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 315 331 7 (POTENTIAL).
FT DOMAIN 332 401 CYTOPLASMIC (POTENTIAL).
FT LIPID 354 354 PALMITATE (POTENTIAL).
FT CARBOHYD 9 9 POTENTIAL.
FT CARBOHYD 12 12 POTENTIAL.
FT CARBOHYD 34 34 POTENTIAL.
FT CARBOHYD 41 41 POTENTIAL.
FT CARBOHYD 49 49 POTENTIAL.
SQ SEQUENCE 401 AA; 45045 MW; 5673B9B8 CRC32;

Query Match 58.1%; Score 1650; DB 1; Length 401;
Best Local Similarity 65.9%; Pred. No. 1.71e-302;
Matches 205; Conservative 54; Mismatches 49; Indels 3; Gaps 3;

Db 71 AIIIMALYSIVCVVGLFGNFLVMYVIVRYTKMKTATNIYIFNFALADALATSTLPFQSVN 130
QY 59 PVIITAVYSVVFVGLVGNLSLVMFVIRYTKMKTATNIYIFNLADALVTTMPFQSAV 118

Db 131 YLMGTWPFGTILCKIVISIDYNNMFTSIETLCTMSVDRIYAVCHPVKALDFTPRNAKII 190
QY 119 YLMNSWPFQDVLCIKIVISIDYNNMFTSIETLTMMMSVDRIYAVCHPVKALDFTPLKAKII 178

Db 191 NICNWILSSAIGLPVFMFMATTKYRQ-S-IDSTLTFSHPTW-YWENLLKICVFIFAFIMP 247
QY 179 NICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWWDLEFMKICVFVFAFVIP 238

Db 248 ILIITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVAVFVVCWTPPIHIYVIAKA 307
QY 239 VLIITVCYTLMLRLKSVRLLSGSREKDRNLRRITKLVLVVAVFIICWTPPIHIFILVEA 298

Db 308 LITIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFRFCPTSTTIEQQNST 367
QY 299 LGSTSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFFCIKMRMERQSTN 358

Db 368 RIRQNTDRHPS 378
QY 359 RVRNTVQDPAS 369
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QY 51 SAHISPAIPVITITAVYSVVVGLVGNLSLVMEFVIIRYTKMKTATNIYIFNLALADALVTT 110

Db 103 TLPFQGTDILLGFWPEGNALCKTVIAIDYNNMETSTFILTAMSVDRYVAICHPIRALDVR 162  
|:|:|:|: |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: |

QY 111 TMPFQSAVYLMNSWPFGLCKIVISIDYNNMETSIFTLTNMSVDRIAVCHPVKALDER 170

Db 163 TSSKAQAVNVAIWALASVVGVPVAIMGSAQV-EDEE-IECLVEIPTQDY-WGPVFA-IC 218  
|:|:|:|: |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: |

QY 171 TPIKAKIINICIWLLASSVGI SAIVLGGTKVREDVDVIECSIQFPD-DEYSWDLFMKIC 229

Db 219 IFLFSPIVPVLVISVCYSIMIRLRGVRLLSGSREKDRNLRRITRLVLVVAVFVGCWTP 278  
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 230 VFVFAFVIPVLIIVCYTILMILRLKSVRLLSGSREKDRNLRRITKILVLVVAVFIICWTP 289

Db 279 VQVFVLAQGLGVQPSSETAVAILRECTALGYVNSCLNPILYAFLDENFKACFRKFCCASA 338  
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

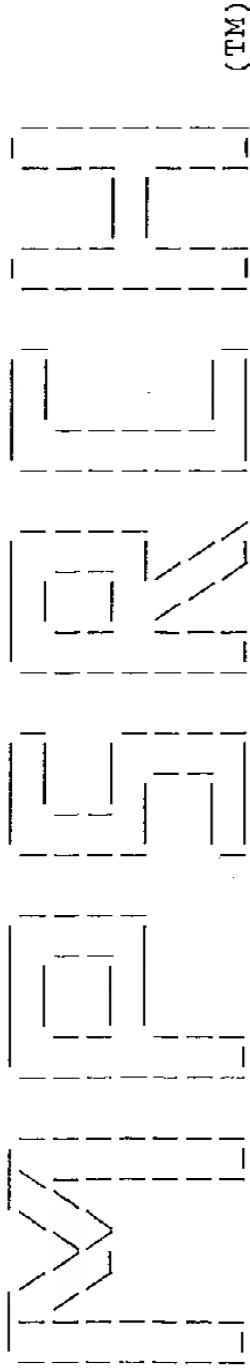
QY 290 IHIFILVEALGSTSHSTAALSSYFICIALGYTNSSSLNPVLVAFLDENFKRCFRDFCFPIK 349

Db 339 LRRDVQVSDRVRSLAKDVA 357  
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QY 350 MRMERQSTNVRNRTVQDPA 368

Search completed: Thu Feb 17 11:13:17 2000  
Job time : 16 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Feb 17 11:13:35 2000; MasPar time 27.84 Seconds  
Tabular output not generated. 745.004 Million cell updates/sec

Title: >US-08-455-683-2  
Description: (1-380) from US08455683.pep  
Perfect Score: 2839  
Sequence: 1 MESPIQIFRGDPGPTCPSA.....RNTVQDPASMRDVGGMKNKPV 380

Scoring table: PAM 150  
Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: sptrembl9  
1:sp\_archaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle  
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified  
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 48.857; Variance 122.078; scale 0.400

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1687	59.4	373	13	O57585	OPIOID RECEPTOR HOMO	1.07e-252
2	1652	58.2	383	13	O42324	MU-OPIOID RECEPTOR.	8.81e-247
3	860	30.3	117	11	Q60733	OPIOID RECEPTOR, KAPPA	2.26e-114
4	662	23.3	119	11	Q64206	DELTA OPIOID RECEPTOR/	4.66e-82
5	613	21.6	371	11	O88854	GALANIN RECEPTOR TYPE	3.70e-74
6	610	21.5	387	4	O43603	GALANIN RECEPTOR GALR2	1.12e-73
7	595	21.0	353	13	O93247	CXCR4.	2.87e-71
8	588	20.7	352	6	O77776	CHEMOKINE RECEPTOR CCR	3.79e-70
9	576	20.3	352	6	O18770	CCR5 RECEPTOR (FRAGMEN	3.16e-68
10	575	20.3	352	4	O15538	CCR5 RECEPTOR (FRAGMEN	4.56e-68
11	572	20.1	359	11	O55169	RECEPTOR PROTEIN CKR3.	1.38e-67
12	569	20.0	383	14	Q89609	G PROTEIN-COUPLED RECE	4.15e-67
13	564	19.9	352	6	O18772	CCR5 RECEPTOR (FRAGMEN	2.61e-66
14	565	19.9	359	11	O54814	CHEMOKINE RECEPTOR CCR	1.81e-66
15	563	19.8	352	6	O18771	CCR5 RECEPTOR (FRAGMEN	3.77e-66
16	547	19.3	374	13	O57466	G PROTEIN COUPLED P2Y	1.34e-63
17	545	19.2	357	13	O42445	CXC CHEMOKINE RECEPTOR	2.78e-63
18	535	18.8	360	6	O18793	CHEMOKINE RECEPTOR.	1.08e-61
19	532	18.7	353	13	P79960	MESENCHYME-ASSOCIATED	3.24e-61
20	532	18.7	373	11	O55193	CHEMOKINE RECEPTOR CCR	3.24e-61

21	527	18.6	465	5	O44426	CARDIOEXCITATORY RECEP	2.01e-60
22	519	18.3	344	6	O77833	CHEMOKINE RECEPTOR CCR	3.73e-59
23	513	18.1	263	5	O76873	EG:121E7.2 PROTEIN.	3.32e-58
24	515	18.1	333	4	O14694	CCR5 RECEPTOR (FRAGMEN	1.60e-58
25	514	18.1	361	11	O35811	G-PROTEIN COUPLED RECE	2.30e-58
26	505	17.8	370	4	O75194	HUMAN PROLACTIN-RELEAS	6.10e-57
27	505	17.8	678	5	O94736	TACHYKININ-LIKE RECEPT	6.10e-57
28	500	17.6	368	4	O60755	GALANIN 2 RECEPTOR HOM	3.76e-56
29	488	17.2	367	11	O54689	G PROTEIN-COUPLED RECE	2.92e-54
30	489	17.2	370	11	O88853	GALANIN RECEPTOR TYPE	2.03e-54
31	486	17.1	370	4	O15132	P2Y5-LIKE RECEPTOR.	6.03e-54
32	482	17.0	360	4	O60835	CXCR4 GENE ENCODING RE	2.57e-53
33	483	17.0	370	11	O88626	GALANIN RECEPTOR TYPE	1.79e-53
34	479	16.9	352	6	O77488	CXCR4 RECEPTOR.	7.60e-53
35	481	16.9	372	13	O93237	CXC CHEMOKINE RECEPTOR	3.69e-53
36	476	16.8	303	13	P70058	ANGIOTENSIN RECEPTOR R	2.25e-52
37	477	16.8	429	5	P92045	LYMNOKININ RECEPTOR.	1.57e-52
38	465	16.4	370	11	O54914	GALANIN RECEPTOR TYPE	1.19e-50
39	464	16.3	399	11	O88790	BOMBESIN RECEPTOR SUBT	1.71e-50
40	463	16.3	399	11	O54798	BOMBESIN-LIKE RECEPTOR	2.45e-50
41	451	15.9	168	11	O35715	SOMATOSTATIN RECEPTOR	1.84e-48
42	449	15.8	378	11	O08707	CHEMOKINE (C-C) RECEPT	3.78e-48
43	447	15.7	390	11	O54799	NEUROMEDIN B RECEPTOR.	7.74e-48
44	442	15.6	238	13	O92158	ANGIOTENSIN II RECEPTO	4.66e-47
45	438	15.4	343	11	O88537	N-FORMYLPEPTIDE RECEPT	1.95e-46

ALIGNMENTS

RESULT 1  
ID O57585 PRELIMINARY; PRT; 373 AA.  
AC O57585;  
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
DE OPIOID RECEPTOR HOMOLOGUE.  
OS BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;  
OC TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;  
OC CYPRINIDAE; RASBORINAE; DANIO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA BARRALLO A., GONZALEZ-SARMIENTO R., GARCIA-MALVAR F., RODRIGUEZ R.E.;  
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
DR EMBL; AJ001596; E1217996; -  
DR PROSITE; PS00237; G-PROTEIN\_RECEPTOR; 1.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.  
SQ SEQUENCE 373 AA; 42520 MW; E900D477 CRC32;

Query Match 59.4%; Score 1687; DB 13; Length 373;  
Best Local Similarity 65.6%; Pred. No. 1.07e-252;  
Matches 206; Conservative 62; Mismatches 42; Indels 4; Gaps 4;

Db	51	IAISITALYSVICVGLGNILVMGVVRYTKLTKTATNIYIFNLALADALATSTLFPQST	110
QY	58	IPVITAVYSVVFVGLVGNLSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTTFQSA	117
Db	111	KYLMNTWPFGEELCKVVIADLYNMFTSIFTLTMMSDRYIAVCHPVRALERTPIKAKI	170
QY	118	VYLMNSWPFGDVLCIVISIDYNMFTSIFTLTMMSDRYIAVCHPVKALDERTPLKAKI	177
Db	171	INVCIWILSSAVGVPIMIMAVIRVTNQNTTV-CMLKFPDPDW-YWDTVTKICVFIFAFVW	228
QY	178	INCIWLLASSVGISAIVLGKTKVREDVDVIECSLOFPDDEYSWDLFMKICVFVFAFVI	237
Db	229	PVLVIICCYGLMILRLKSVRLSGSKEKDRNMRRTMRVVLVVAAFIICWTPIHIFIEK	288
QY	238	PVLIIIVCYTLMILRLKSVRLSGSREKDRNLRRTIKLVVVAVFIICWTPIHIFILVE	297
Db	289	TLVDINQKNPFVIAASWHLHRT-GYTNSSLNPLVYAPLDENFKRCFRDLCPLPFRADQSN	347
QY	298	ALGSTSHSTA-AISSYFCIALGYTNSSLNPLVYAPLDENFKRCFRDLCPLPFRADQSN	356



OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SV;  
RA KOLAKOWSKI L.F. JR., BROUSSARD S.R.;  
RT "Galanin Receptor Type 2 (Galr2) from Human and Mouse: Genomic  
RT Cloning, Chromosomal Localization, Functional Expression, Gq  
RT Dependent Signal Transduction, and Expression Pattern.";  
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBBJ DATA BANKS.  
DR EMBL; AF042784; G3642918; -.  
SQ SEQUENCE 371 AA; 40533 MW; FF7FBA0C CRC32;  
  
Query Match 21.6%; Score 613; DB 11; Length 371;  
Best Local Similarity 29.5%; Pred. No. 3.70e-74;  
Matches 97; Conservative 108; Mismatches 111; Indels 12; Gaps 10;  
  
Db 2 NGSDSQGAEDSSQEGGGWQPEAVLPLFFALIFLVGAVGNALVLAALLRGGAQVSTTNL 61  
QY 37 DSNQSVGSEDQQLSAHISPAIPVIITAVYSVVFVGLVGNLSVMFVIIRYTKMKIATNI 96  
  
Db 62 FILNLGVADLCFILCCVPFQATVITLDDWVFGSLCKKAVHFLIFLTMHASSFTLAASVLD 121  
QY 97 YIFNLALADA-LVTTTTFQSAVYLMNSWPFQDVLCIKIVISIDYNNMFTSIFTLTMMMSVD 155  
  
Db 122 RYLAIRYPMHSRELRTPRNALAAIGL-IWGLAL-L-FSGPYLSYYSQSOLANLIVCHPAW 178  
QY 156 RYIAVCHPVKALDFRTPLKA-KIINICIWLLASSVGISAIVLGGTKVREDVDVIECSLQF 214  
  
Db 179 SAP--RRRA--MDLCTFVFSYLLPVLVLSLYA-RTLHYLWRTVDPVAAGSGSQRARKV 233  
QY 215 PDDEYSWDLFMKICVFVFAFVPIVLIIVCYTLMILR-L-KSVRLSGSREKDRNLRI 272  
  
Db 234 TRMIVIVAVLFCLOWMPHHLICVWFGRFPLTRAIYALRIILSHLVSYANSCVNPVVAL 293  
QY 273 TKLVLVVAVVFIICWTPIHIFILVEALGSTSHSTAALSSYFICIALGYTNSLNPVLYAF 332  
  
Db 294 VSKHFRKGFRKICAGLLRRAPRRASGRV 321  
QY 333 LDENFKRCFRDFCFPIKMRMERQSTNRV 360  
  
RESULT 6  
ID O43603 PRELIMINARY; PRI; 387 AA.  
AC O43603;  
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
DE GALANIN RECEPTOR GALR2.  
GN GALNR2 OR GALR2.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
OC CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 98153789.  
RA BLOOMQUIST B.T., BEAUCHAMP M.R., ZHELNIN L., BROWN S.-E.,  
RA GORE-WILLSE A.R., GREGOR P., CORNFIELD L.J.;  
RT "Cloning and expression of the human galanin receptor Galr2.";  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 243:474-479(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA FAITHI Z., BATTAGLINO P.M., IBEN L.G., LI H., BAKER E., ZHANG D.,  
RA MCGOVERN R., MAHLE C.D., SUTHERLAND G.R., IISMAA T.P.,  
RA DICKINSON K.E.J., ANTAL ZIMANYI I.;  
RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBBJ DATA BANKS.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA KOLAKOWSKI L.F. JR., BROUSSARD S.R.;  
RT "Galanin Receptor Type 2 (Galr2) from Human and Mouse: Genomic  
RT Cloning, Chromosomal Localization, Functional Expression, Gq  
RT Dependent Signal Transduction, and Expression Pattern."  
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBBJ DATA BANKS.  
DR EMBL; AF040630; G2921760; -.

DR EMBL; AF058762; G3170599; -.  
DR EMBL; AF042782; G3642914; -.  
SQ SEQUENCE 387 AA; 41700 MW; E7A343C3 CRC32;  
  
Query Match 21.5%; Score 610; DB 4; Length 387;  
Best Local Similarity 31.4%; Pred. No. 1.12e-73;  
Matches 96; Conservative 99; Mismatches 99; Indels 12; Gaps 10;  
  
Db 25 AVIVPELLFALIFLVGTGNTLVLAALLRGGAQVSTTNLFILNLGVADLCFILCCVPFQAT 84  
QY 59 PVIITAVYSVVFVGLVGNLSVMFVIIRYTKMKIATNIYIFNLALADA-LVTITMPFQSA 117  
  
Db 85 IYTLDGWVFGSLCKKAVHFLIFLTMHASSFTLAASVLDRIYLAIRYPLHSRELRTPRNALA 144  
QY 118 VYLMNSWPFQDVLCIKIVISIDYNNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLKA-K 176  
  
Db 145 AIGL-IWGL-SLL-FSGPYLSYYSQSOLANLIVCHPAWSAP--RRRA--MDICTFVSYL 197  
QY 177 IINICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFV 236  
  
Db 198 LPVLVLGLTYA-RTLRYLWRAVDPVAAGSGARRAKRKVTRMILIVAAFLCLOWMPHHLI 256  
QY 237 IPVLIIVCYTLMILR-L-KSVRLSGSREKDRNLRIITKLVLVVAVFIICWIPIHIFI 294  
  
Db 257 LCVWFGQFPLTRAIYALRIILSHLVSYANSCVNPVYALVSKHFRKGFRTICAGLLRAPG 316  
QY 295 LVEALGSTSHSTAALSSYFICIALGYTNSLNPVLYAFLDENFKRCFRDFCFPIKMRMER 354  
  
Db 317 RASGRV 322  
QY 355 QSTNRV 360  
  
RESULT 7  
ID O93247 PRELIMINARY; PRI; 353 AA.  
AC O93247;  
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
DE CXCR4.  
OS CYPRINUS CARPIO (COMMON CARP).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;  
OC TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;  
OC CYPRINIDAE; CYPRININAE; CYPRINUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA FUJIKI K., NAKAO M., SHIN D., YANO T.;  
RT "CDNA cloning of a carp homologue of mammalian CXCR4."  
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBBJ DATA BANKS.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AB012310; D1033763; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.  
SQ SEQUENCE 353 AA; 39633 MW; 23DD5347 CRC32;  
  
Query Match 21.0%; Score 595; DB 13; Length 353;  
Best Local Similarity 30.3%; Pred. No. 2.87e-71;  
Matches 107; Conservative 102; Mismatches 120; Indels 24; Gaps 18;  
  
Db 11 NSSDSGSGDFDFDELCDLKVSNDFOKIFLPVYGIIFVLGIIGNGLVVLVMGFOKSKNM 70  
QY 35 ESDNSGVSSEDQQLSAHISPAIP-VIITAVYSVVFVGLVGNLSVMFVIIRYTKMKA 93  
  
Db 71 TDKYRLHLSIADLLFVJTLPP-WAVDAASGWHFEGGFLC-VTVNMIYTLNLYSSVLIIFI 128  
QY 94 TNYIFNLALADALVTITMPFQSAVYLMNSWPFQDVLCIKIVISIDY-YNMFTSIFTLMM 152  
  
Db 129 SLDRYLAVVRATNSQNFRRVLAEKVIYLGWLPASILLVTPDLVF--AKVHDTGMNTI-CE 185  
QY 153 SVDRYIAVCHPVKALDFRTPLKAKIINICIWLLASSVGSISAIVLGGTKVRE-DVDVIECS 211  
  
Db 186 LTYPLQGNTVWKAVERFQHFIV-GFLLPLGLIILTCYCIISKL-S-KNSKGQALKRKALK 242



QY 110 TTMFPQSAVILMNSWPFQDVLCCKIVISIDYNNMFTSIFILTMMSVDRIYAVCHPVKALDF 169  
Db 140 RIVTFGVVTSVITWVAVFASLPGLGFIIFRSQ-KEGLHYI-CSSHFPYSQYQFWKNEQTLK 197  
QY 170 RIPLKAKIINICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWWDLFMKIC 229  
Db 198 IVILGLVPLLVVICYS-GIL--KT--LLRCRNEKKRH-RAV-RLIFTIMIVYFLFWAP 250  
QY 230 VVFAFVIPVLIIVCYTLMILRLKSVRLLSGSRKDRNLRRITKLVVVAVFIICWTP 289  
Db 251 YNIVLLNTFOEFFGLNCCSSNRLDQAMQVTEITGMTHCCINPIIYAFVGEKERNYLLV 310  
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYFFCIALGYTNSSLNPVLYAFLDENFKRCFRD 343  
Db 311 F 311  
QY 344 F 344

RESULT 11  
ID O55169 PRELIMINARY; PRT; 359 AA.  
AC O55169;  
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE RECEPTOR PROTEIN CKR3.  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;  
OC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WTSTAR; TISSUE=SPLEEN;  
RA HARRINGTON P.M., NEWTON D.J., COLEMAN J.W., FLANAGAN B.F.;  
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; Y13400; E1247073; -.  
SQ SEQUENCE 359 AA; 41609 MW; 874DF714 CRC32;

Query Match 20.1%; Score 572; DB 11; Length 359;  
Best Local Similarity 31.3%; Pred. No. 1.38e-67;  
Matches 91; Conservative 92; Mismatches 90; Indels 18; Gaps 14;

Db 40 LLPLYSLVFIVGLLGNMVMVLLILIKYRKLQIMTNIYLLNLAISDLLFLTVPF-WIHVV 98  
QY 61 IITAVYSVVFVVGVLGNSLVMEVIIRYIKMKTATNIYIFNLALADALVTTMPFQSAVYL 120  
Db 99 LWNWGFCHCMCKMLSGLYIALYSEIFFIILLTIDRYLAIVHAVLALRARIVTFALITS 158  
QY 121 M-NSWPFQDVLCCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKIIN 179  
Db 159 IITWGLAVLAALPEFIFHES--QDNFGDLSCSRPRYEGEEDSWKRFHALRMNIFGLALPL 216  
QY 180 ICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWWDLFMKICVFFAFVTPV 239  
Db 217 LIMVICYS-GIL--KT--LLR-CPNKKKH-KAI-QLIFVVMIVFFEIFWTPYNLVLLLSAF 268  
QY 240 LIIIVCYTLMILRLKSVRLLSGSRKDRNLRRITKLVVVAVFIICWTPIH-IFIL-V- 296  
Db 269 HSTFLETSCQOSIHLDLAMOQVTEVITHTHCCINPIIYAFGERFRKHLRLF 319  
QY 297 EA--LGSTSHSTAALS-SYFFCIALGYTNSSLNPVLYAFLDENFKRCFRDE 344

RESULT 12  
ID Q89609 PRELIMINARY; PRT; 383 AA.  
AC Q89609;  
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
DE G PROTEIN-COUPLED RECEPTOR.  
OS EQUINE HERPESVIRUS TYPE 2 (EHV-2).  
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;  
OC BETAHERPESVIRINAE.

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=86/67;  
RX MEDLINE; 95302501.  
RA TELFORD E.A., WATSON M.S., AIRD H.C., PERRY J., DAVIDSON A.J.;  
RT "The DNA sequence of equine herpesvirus 2.";  
RL J. MOL. BIOL. 249:520-528(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=86/67;  
RA TELFORD E.A.R.;  
RL SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; U20824; G695251; -.  
DR EMBL; U20824; G695173; -.  
DR PFAM; PF00001; 7tm\_1; 1.  
SQ SEQUENCE 383 AA; 43667 MW; 60F5BFDD4 CRC32;

Query Match 20.0%; Score 569; DB 14; Length 383;  
Best Local Similarity 31.3%; Pred. No. 4.15e-67;  
Matches 90; Conservative 97; Mismatches 80; Indels 21; Gaps 16;

Db 74 VVPALYLLVFLFGLLGNILVVIIRYMKIKNLTNMLLNLAISDLLFLTLPF-WMHVI 132  
QY 61 IITAVYSVVFVVGVLGNSLVMEVIIRYIKMKTATNIYIFNLALADALVTTMPFQSAVYL 120  
Db 133 GMYHDWTFGISLCKLLRGVCYMSLYSQVFCIILLTVDRYIAVVYAVTALFRVTTCGIYT 192  
QY 121 -M-NSWPFQDVLCCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPLKAKII 178  
Db 193 CVCTWFLAGLLSLPEFFHG-H-QDDNGRVQCDPYYPENSTNVWRRHAVK-VIMLSLIL 249  
QY 179 NICIWLASSVGISAIVLGGTKVREDVDVIECSLQFPD-DEYSWWDLFMKICVFFAFVI 237  
Db 250 PLLIMAVCY-YVIIR---RLLR--RPSKKKYKAI-RLIFVIMVAYFVFWTPYNIIVLLIS 301  
QY 238 PVLIIIVCYTLMILRLKSVRLLSGSRKDRNLRRITKLVVVAVVAVFIICWTPIHIFILVE 297  
Db 302 TFHAILLNQCALSSNLDMLLITKTVAYTHCCINPVIYAFVGEKFR 349  
QY 298 ALGST--S-H-S-TAALS-SYFFCIALGYTNSSLNPVLYAFLDENFKR 339

RESULT 13  
ID O18772 PRELIMINARY; PRT; 352 AA.  
AC O18772;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
DE CCR5 RECEPTOR (FRAGMENT).  
GN CCR5.  
OS PAN TROGLODYTES (CHIMPANZEE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
OC CAIARRHINI; HOMINIDAE; PAN.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CHCCR5-142A;  
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,  
RA HO D.D.;  
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).  
DR EMBL; AF011541; G2305200; -.  
DR PFAM; PF00001; 7tm\_1; 1.  
FT NON\_TER 352 352  
SQ SEQUENCE 352 AA; 40598 MW; A9BF8EDF CRC32;

Query Match 19.9%; Score 564; DB 6; Length 352;  
Best Local Similarity 28.2%; Pred. No. 2.61e-66;  
Matches 85; Conservative 100; Mismatches 100; Indels 16; Gaps 14;  
Db 21 QKINVQIAARLLPPLYSLVFIFGFVDNMLVILLINCKRLKSMTDIYLLNLAISDLFFL 80  
QY 50 ESAHISPAIPVIITAVYSVVFVVGVLGNSLVMEVIIRYIKMKTATNIYIFNLALADALVT 109  
Db 81 LTVPF-WAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAIVHAVFAKKA 139

QY 110 TTMPEQSAVYLMNSWPEGDVLCCKIVISIDYNNMETSIFTLTMSVDRIYAVCHPVKALDF 169  
Db 140 RTVTFGVVTSVITWVAVFASLPGLGIIFTRSQ-KEGLHYT-CSSHFPYSQYQFWKNFQTLK 197  
QY 170 RTPLKAKIINICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWWDLFMKIC 229  
Db 198 IVILGLVPLLVVICYS-GIL--KT--LLRCRNEKKRH-RAV-RLIFTMIVYFLFWAP 250  
QY 230 VVFAFVPIPVLIIVCYTLMILRLKSVRLSSREKDRNLRRITKLVVVAVFIIICWTP 289  
Db 251 YDIVLLNTFQEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAFVGEKFRNYLLV 310  
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYYFCIALGYTNSSLNPVLYAFLDENFKRCFRD 343  
Db 311 F 311  
QY 344 F 344  
RESULT 14  
ID Q54814 PRELIMINARY; PRT; 359 AA.  
AC Q54814;  
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE CHEMOKINE RECEPTOR COR3.  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;  
OC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WISTAR; TISSUE=SPLEEN;  
RA JIANG Y., SALAFRANCA M.N., ADHIKARI S., XIA Y., FENG L., SONNTAG M.K.,  
RA DEFIEBRE C.M., PENNELL N.A., STREIT W.J., HARRISON J.K.;  
RL J. NEUROIMMUNOL. 0:0-0(1998).  
DR EMBL; AF003954; G2897073; -.  
SQ SEQUENCE 359 AA; 41643 MW; C1FC70CA CRC32;

Query Match 19.9%; Score 565; DB 11; Length 359;  
Best Local Similarity 30.9%; Pred. No. 1.81e-66;  
Matches 90; Conservative 93; Mismatches 90; Indels 18; Gaps 14;  
Db 40 LLPPLYSLVFIIVGLGNMVMVLILIKYRKLIQIMTNIYLLNLAISDLLFLFTVPPF-WIHVV 98  
QY 61 IITAVYSVVFVVGVLGNSLVMFVLIIRYTKMKTATNIYIFNLALADALVTTTTPFQSAVYL 120  
Db 99 LWNWEGFGCHCMKMLSLGLYLYALYSEIFFIILLTIDRYLAIVHAVLALRARIVTFATITS 158  
QY 121 M-NSWPFQGDVLCCKIVISIDYNNMETSIFTLTMSVDRIYAVCHPVKALDFRIPLKAKIIN 179  
Db 159 IITWGFVLAALPEFIFHES--QDNFGDLSCSPRYPEGEEDSWKRHFALRMNIFGLALPL 216  
QY 180 ICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWWDLFMKICVFAFVPIV 239  
Db 217 LTMVICYS-GII--KT--LLR-CPNKKH-KAI-QLIFVVMIVFFIFWTPYNLVLLLSAF 268  
QY 240 LIIIVCYTLMILRLKSVRLSSREKDRNLRRITKLVVVAVFIIICWTPIH-IFIL-V- 296  
Db 269 HSTFLETSCQQSIHLDLAMQVTEVITHTHCCINPIIYAFVGERFRKHLRLF 319  
QY 297 EA--LGSTSHSTAALS-SYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDE 344

RESULT 15  
ID Q18771 PRELIMINARY; PRT; 352 AA.  
AC Q18771;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
DE CCR5 RECEPTOR (FRAGMENT).  
GN CCR5.  
OS PAN TROGLODYTES (CHIMPANZEE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
OC CATARRHINI; HOMINIDAE; PAN.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CHCCR5-141A;  
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,  
RA HO D.D.;  
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).  
DR EMBL; AF011539; G2305196; -.  
PFAM; PF00001; 7cm\_1; 1.  
FT NON\_TER 352 352  
SQ SEQUENCE 352 AA; 40466 MW; D52C67E1 CRC32;  
Query Match 19.8%; Score 563; DB 6; Length 352;  
Best Local Similarity 27.9%; Pred. No. 3.77e-66;  
Matches 84; Conservative 102; Mismatches 99; Indels 16; Gaps 14;  
Db 21 QKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISNLFEL 80  
QY 50 ESAHISPAIPVITAVYSVVFVVGVLGNSLVMFVLIIRYTKMKTATNIYIFNLALADALVT 109  
Db 81 LTVPF-WAHYAAAQWDFGNTMCQLLTGLYFICFPESGIFFIILLTIDRYLAIVHAVFALKA 139  
QY 110 TTMPEQSAVYLMNSWPEGDVLCCKIVISIDYNNMETSIFTLTMSVDRIYAVCHPVKALDF 169  
Db 140 RTVTFGVVTSVITWVAVFASLPGLGIIFTRSQ-KGGLHYT-CSSHFPYSQYQFWKNFQTLK 197  
QY 170 RTPLKAKIINICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWWDLFMKIC 229  
Db 198 IVILGLVPLLVVICYS-GIL--KT--LLRCRNEKKRH-RAV-RLIFTMIVYFLFWAP 250  
QY 230 VVFAFVPIPVLIIVCYTLMILRLKSVRLSSREKDRNLRRITKLVVVAVFIIICWTP 289  
Db 251 YNIVLLNTFQEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAFVGEKFRNYLLV 310  
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYYFCIALGYTNSSLNPVLYAFLDENFKRCFRD 343  
Db 311 F 311  
QY 344 F 344

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(without alignments)  
-2629.655 Million cell updates/sec

Title: US-08-455-683-11  
Perfect score: 1000  
Sequence: 1 AAGAAGCAAAATCAGTAATC.....CCAGTATGACTAGTCGTGGA 1000

Scoring table: OLIGO\_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:\*

Word size : 0

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2: gb\_ba2:\*  
3: gb\_om:\*  
4: gb\_ov:\*  
5: gb\_pat:\*  
6: gb\_ph:\*  
7: gb\_pl1:\*  
8: gb\_pl2:\*  
9: gb\_pr1:\*  
10: gb\_pr2:\*  
11: gb\_pr3:\*  
12: gb\_ro:\*  
13: gb\_sts:\*  
14: gb\_sy:\*  
15: gb\_un:\*  
16: gb\_vl:\*  
17: em\_fun:\*  
18: em\_hum1:\*  
19: em\_hum2:\*  
20: em\_in:\*  
21: em\_om:\*  
22: em\_or:\*  
23: em\_ov:\*  
24: em\_pat:\*  
25: em\_ph:\*  
26: em\_pl:\*  
27: em\_ro:\*  
28: em\_sts:\*  
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30: em\_un:\*  
31: em\_vi:\*  
32: gb\_htg1:\*  
33: gb\_htg2:\*  
34: gb\_in1:\*  
35: gb\_in2:\*  
36: em\_bal:\*  
37: em\_ba2:\*  
38: em\_hum3:\*  
39: em\_hum4:\*  
40: gb\_pr4:\*  
41: gb\_htg3:\*  
42: gb\_htg4:\*  
43: gb\_htg5:\*  
44: gb\_htg6:\*  
45: gb\_htg7:\*  
46: em\_htg1:\*  
47: em\_htg2:\*  
48: em\_htg3:\*  
49: em\_hum5:\*

50: gb\_pl3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	455	45.5	455	9	HUMOPRK1A	L26079 Homo sapien
2	439	43.9	1142	5	A48343	A48343 Sequence 1
3	439	43.9	1604	9	HUMOPRK1B	L37362 Homo sapien
4	439	43.9	1154	11	HSU17298	U17298 Human kappa
5	354	35.4	1182	9	HSU11053	U11053 Human kappa
6	252	25.2	183559	42	AC009646	AC009646 Homo sapi
7	221	22.1	1229	9	HSU16860	U16860 Human kappa
8	196	19.6	432	9	HUMKOR	L36130 Homo sapien
9	47	4.7	1733	12	CPU04092	U04092 Cavia porce
10	41	4.1	715	3	AF012105	AF012105 Sus scrof
11	33	3.3	432	12	MMU16998	U16998 Mus musculu
12	33	3.3	488	12	MUSMORGDP2	D31664 Mouse MORGD
13	33	3.3	658	12	RNKOR2	U17994 Rattus norv
14	33	3.3	1109	12	S77868S2	S77869 kappa opioi
15	32	3.2	1408	5	A68828	A68828 Sequence 5
16	32	3.2	2481	5	E08874	E08874 CDNA coding
17	32	3.2	1410	12	MUSKAPOPRE	L11065 Mouse kappa
18	32	3.2	2481	12	RATKOR	D16829 Rattus norv
19	32	3.2	1358	12	RATKOR1A	L22001 Rat kappa o
20	32	3.2	2094	12	RATKOR1B	L22536 Rattus norv
21	32	3.2	1273	12	RATRORD	D15534 Rat mRNA fo
22	32	3.2	4048	12	RNKOR3	U17995 Rattus norv
23	32	3.2	4742	12	RNU00442	U00442 Rattus norv
24	32	3.2	1288	12	S81111	S81111 kappa-opioi
25	29	2.9	686	3	SSU71149	U71149 Sus scrofa
26	29	2.9	2219	5	A38528	A38528 Sequence 1
27	29	2.9	2218	5	A68826	A68826 Sequence 3
28	29	2.9	2272	12	MUSDELOPRE	L11064 Mouse delta
29	29	2.9	2219	12	MUSDELTO	L06322 Mus musculu
30	29	2.9	1835	12	MUSDOPRCP	L07271 Mouse delta
31	29	2.9	1418	12	RATRORA	D16348 Rat mRNA fo
32	29	2.9	1366	12	RNU00475	U00475 Rattus norv
33	29	2.9	1834	12	S65335	S65335 delta opioi
34	29	2.9	2203	12	S66181	S66181 delta opiat
35	29	2.9	356	12	S81965	S81965 delta opioi
36	26	2.6	638	12	MUSMORGDP3	D31665 Mouse MORGD
37	26	2.6	1401	12	RATMOPIOID	L22455 Rat mu opio
38	26	2.6	1586	12	RATMORA	L13069 Rattus norv
39	26	2.6	2135	12	RATMUOR1A	L20684 Rattus norv
40	26	2.6	2397	12	RATRORB	D16349 Rat mRNA fo
41	26	2.6	1448	12	RNU02083	U02083 Rattus norv
42	26	2.6	1367	12	RNU35424	U35424 Rattus norv
43	26	2.6	720	12	S77863	S77863 mu-opioid r
44	26	2.6	1186	12	S77868S3	S77872 kappa opioi
45	25	2.5	2162	9	HUMMOR1X	L25119 Human Mu op

ALIGNMENTS

RESULT	1
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LOCUS	HUMOPRK1A 455 bp DNA
DEFINITION	Homo sapiens (clone hSR4-1) kappa opioid receptor (OPRK1) gene, complete exon.
ACCESSION	L26079
VERSION	L26079.1 GI:415143
KEYWORDS	OPRK1 gene; kappa opioid receptor.
SOURCE	Homo sapiens (tissue library: Stratagene 946203; lambda) male placenta DNA.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE 1 (bases 1 to 455)  
AUTHORS Yasuda,K., Espinosa,R.III., Takeda,J., Le Beau,M.M. and Bell,G.I.  
TITLE Localization of kappa opiod receptor gene to human chromosome band 8q11.2

JOURNAL Unpublished (1994)  
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Db 301 GCGIGGACCGCTACATTGCCGTGTGCCACCCCGTGAAGGCTTTGGACTTCGGCACACCCCT 360  
  
QY 361 TGAAGGCAAGATCATCAATATCTGCATCTGGCTGCTGTGCGICATCTGTGGCATCTCTG 420  
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Db 361 TGAAGGCAAGATCATCAATATCTGCATCTGGCTGCTGTGCGICATCTGTGGCATCTCTG 420  
  
QY 421 CAATAGTCCTTGGAGGCACCAAGTCAGGGAAGGT 455  
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Db 421 CAATAGTCCTTGGAGGCACCAAGTCAGGGAAGGT 455

RESULT 2  
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LOCUS A48343 1142 bp DNA PAT 07-MAR-1997  
DEFINITION Sequence 1 from Patent WO9601898.  
ACCESSION A48343  
VERSION A48343.1 GI:2302133  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 1142)  
AUTHORS Kieffer,B. and Simonin,F.  
TITLE HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF

JOURNAL

Patent: WO 9601898-A 1 25-JAN-1996;  
UNIV PASTEUR (FR)

COMMENT Other publication FR 2722209 960112.  
FEATURES Location/Qualifiers  
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QY 280 ICTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAAGG 339  
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QY 340 CTTTGGACTTCGGCACACCCCTTGAAAGSCAAAGATCATCAATATCTGCATCTGGCTGTGT 399  
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Db 497 CTTTGGACTTCGGCACACCCCTTGAAAGSCAAAGATCATCAATATCTGCATCTGGCTGTGT 556  
  
QY 400 CGTCAICTGTTGGCATCTCTGCAATAGTCTCTTGGAGGCCACCAAGTCAGGGAAGGTGTCG 459  
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Db 557 CGTCAICTGTTGGCATCTCTGCAATAGTCTCTTGGAGGCCACCAAGTCAGGGAAGACGTGCG 616  
  
QY 460 ATGTCATTTGAGTGTGCTTGCAGTTCCAGATGATGACTACTCTCTGGTGGGACCTCTTCA 519  
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Db 617 ATGTCATTTGAGTGTGCTTGCAGTTCCAGATGATGACTACTCTCTGGTGGGACCTCTTCA 676  
  
QY 520 TGAAGATCGCGTCTTCATCTTTGCCCTTCGTGATCCCTGTCTCATCATCATCGTCTGCT 579  
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Db 677 TGAAGATCGCGTCTTCATCTTTGCCCTTCGTGATCCCTGTCTCATCATCATCGTCTGCT 736  
  
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Db 737 ACACCCCTGATGATCCTGCGTCTCAAGAGCGTCCGGCTCCCTTCTGGCTCCCGAGAGAAAG 796  
  
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QY 700 GCTGGACTCCCATTCACATATTCATCTGTTGGAGGCTCTGTTGGGAGCACCTCCACACAGCA 759  
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Db 857 GCTGGACTCCCATTCACATATTCATCTGTTGGAGGCTCTGTTGGGAGCACCTCCACACAGCA 916  
  
QY 760 CAGCTGCTCTCTCCAGCTATTACTTCTGTCATCGCCTTAGGCTATACCAACAGTAGCCTGA 819  
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QY	880	ITCCACTGAGATGAG	895
Db	1037	ITCCACTGAGATGAG	1052
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DEFINITION	Homo sapiens (clone d2-115) kappa opioid receptor (OPRK1) mRNA, complete cds.		22-MAR-1995
ACCESSION	L37362		
VERSION	L37362.1	GI:722617	
KEYWORDS	OPRK1 gene; kappa opioid receptor; opioid receptor.		
SOURCE	Homo sapiens (clone d2-115) (tissue library: genomic in lambda dash and cDNA in lambda ZAPII) fetus brain cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Zhu,J., Chen,C., Xue,J.-C., Kunapuli,S., Dieriel,J.K. and Liu-Chen,L.-Y.		
TITLE	Cloning of a human .kappa. opioid receptor from the brain		
JOURNAL	Life Sci. 56, 201-207 (1995)		
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		0; Gaps	0;
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QY	220	TTGGGGATGTGCTGIGCAAGATAGTAATTTCCATTGATTACTACAACATGTTCCACCAGCA	279

Db	754	TTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAACATGTTCCACCAGCA	813
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QY	340	CTTTGGACTCCGCACACCCCTTGAAGCAAAAGATCATCAATATCTGCATCTGGTGTGCTGT	399
Db	874	CTTTGGACTCCGCACACCCCTTGAAGCAAAAGATCATCAATATCTGCATCTGGTGTGCTGT	933
QY	400	CGTCATCTGTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAGTCAGGGAAGGTGICG	459
Db	934	CGTCATCTGTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAGTCAGGGAAGACGTGCG	993
QY	460	ATGTCATGAGTGTGCTGCTTGCAGTCCAGATGATGACTACTCTCTGGTGGGACCTCTTCA	519
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QY	820	ATCCCATCTCTACGCCCTTTCTTGATGATAAACTTCAAGCGGTGTTTCCGGGACTTCTGCT	879
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QY	880	TTCCACTGAAGATGAG	895
Db	1414	TTCCACTGAAGATGAG	1429
RESULT	4		
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LOCUS	HSU17298	1154 bp	mRNA
DEFINITION	Human kappa opioid receptor (hKOR) mRNA, complete cds.		14-JUL-1995
ACCESSION	U17298		
VERSION	U17298.1	GI:596069	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Simonin,F., Gaveriaux-Ruff,C., Befort,K., Matthes,H., Lannes,B., Micheletti,G., Mattei,M.G., Charron,G., Bloch,B. and Kieffer,B.		
TITLE	Kappa-Opioid receptor in humans: cDNA and genomic cloning, chromosomal assignment, functional expression, pharmacology, and expression pattern in the central nervous system		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 92 (15), 7006-7010 (1995)		
MEDLINE	95350200		
REFERENCE	2		
AUTHORS	Manesson,E., Bare,L. and Yang,D.		
TITLE	Isolation of a human kappa opioid receptor cDNA from placenta		
JOURNAL	Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)		
MEDLINE	94338360		
AUTHORS	Kieffer,B.		





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similar to mouse kappa type opioid receptor, SwissProt
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Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 295 TGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAGGCTTTGGACTTCGCA 354
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QY 355 CACCCCTGAAGGCAAGATCATCAATATCTGCATCTGGCTGCTGTCATCTGTGGCA 414
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QY 415 TCCTGCAATAGTCCTTGGAGGCACCAAAAGTCAGGGAAGGT 455
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Db 181 TCCTGCAATAGTCCTTGGAGGCACCAAAAGTCAGGGAAGGT 221
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RESULT 8
HUMKOR
LOCUS HUMKOR 432 bp mRNA PRI 13-MAR-1995
DEFINITION Homo sapiens kappa opiate receptor mRNA, partial cds.
ACCESSION L36130
VERSION L36130.1 GI:598184
KEYWORDS kappa opiate receptor.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 432)
AUTHORS Wang,J.B., Johnson,P.S., Wu,J.M., Wang,W.F. and Uhl,G.R.
TITLE Human kappa opiate receptor second extracellular loop elevates
dynorphin's affinity for human mu/kappa chimeras
JOURNAL J. Biol. Chem. 269 (42), 25966-25969 (1994)
MEDLINE 95014415
FEATURES
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CDS
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Best Local Similarity 100.0%; Pred. No. 1.3e-99;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 318 GCCGTGTGCCACCCCGTGAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAGATCATC 377
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Db 70 GCCGTGTGCCACCCCGTGAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAGATCATC 129
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QY 378 AATATCTGCATCTGGCTGCTGTCGTCATCTGTGGCATCTCTGCAATAGTCTTGAGGC 437
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Db 130 AATATCTGCATCTGGCTGCTGTCGTCATCTGTGGCATCTCTGCAATAGTCTTGAGGC 189
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QY 438 ACCAAAGTCAGGGAAG 453
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Db 190 ACCAAAGTCAGGGAAG 205
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RESULT 9
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LOCUS CPU04092 1733 bp mRNA ROD 24-MAY-1995
DEFINITION Cavia porcellus Hartley kappa opioid receptor mRNA, complete cds.
ACCESSION U04092
VERSION U04092.1 GI:476106
KEYWORDS guinea pig.
SOURCE Cavia porcellus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE 1 (bases 1 to 1733)
AUTHORS Xie,G.X., Meng,F., Mansour,A., Thompson,R.C., Hoversten,M.T.,
Goldstein,A., Watson,S.J. and Akil,H.
TITLE Primary structure and functional expression of a guinea pig kappa
opioid (dynorphin) receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (9), 3779-3783 (1994)
MEDLINE 94224825
REFERENCE 2 (bases 1 to 1733)
AUTHORS Xie,G.
TITLE Direct Submission
JOURNAL Submitted (07-DEC-1993) Guo-xi Xie, Mental Health Research
Institute, The University of Michigan, 205 Zina Pitcher Place, Ann
Arbor, MI 48109-0720, USA
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TITLE Structure and chromosomal mapping of genes for the mouse  
kappa-opioid receptor and an opioid receptor homologue (MOR-C)  
JOURNAL Biochem. Biophys. Res. Commun. 205 (2), 1353-1357 (1994)  
MEDLINE 95100967  
REFERENCE 2 (bases 1 to 488)  
AUTHORS Takeshima, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi  
Takeshima, Tokyo Institute of Psychiatry, Department of  
Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan  
(Tel:03-3304-5701(ex.312), Fax:03-3329-8035)  
COMMENT Submitted (28-May-1994) to DDBJ by:  
Hiroshi Takeshima  
Department of Neurochemistry  
Tokyo Institute of Psychiatry  
2-1-8 Kamikitazawa, Setagaya-ku  
Tokyo 156  
Japan  
Phone: 03-3304-5701 x312  
Fax: 03-3329-8035.  
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ACCESSION U17994  
VERSION U17994.1 GI:727257  
KEYWORDS  
SEGMENT 2 of 3  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 658)  
AUTHORS Yakovlev, A.G., Krueger, K.E. and Faden, A.I.  
TITLE Structure and expression of a rat kappa opioid receptor gene  
JOURNAL J. Biol. Chem. 270 (12), 6421-6424 (1995)  
MEDLINE 95204422  
REFERENCE 2 (bases 1 to 658)  
AUTHORS Yakovlev, A.G.  
TITLE Direct Submission  
JOURNAL Submitted (02-DEC-1994) Alexander G. Yakovlev, Georgetown  
University School of Medicine, Neurology, 3900 Reservoir Rd.,  
Washington, DC 20007, USA  
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ACCESSION S77869  
VERSION S77869.1 GI:998530  
KEYWORDS  
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ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1109)  
AUTHORS Liu, H.C., Lu, S., Augustin, L.B., Felsheim, R.F., Chen, H.C., Loh, H.H. and Wei, L.N.  
TITLE Cloning and promoter mapping of mouse kappa opioid receptor gene  
JOURNAL Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)  
MEDLINE 95251663  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 166534] from the original journal article.  
This sequence comes from Fig. 2.  
  
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ACCESSION A68828  
VERSION A68828.1 GI:4759756  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 1408)  
AUTHORS Kieffer, B.L., Matthes, H.W., Simonin, F.H., Dierich, A. and Lemeur, M.  
TITLE TRANSGENIC ANIMAL WHOSE EXPRESSION OF THE OPIATE RECEPTORS IS  
MODIFIED  
JOURNAL Patent: WO 9802534-A 22-JAN-1998;

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FEATURES     Other publication FR 2750825 19980116.
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Job time: 1972 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Perfect score: 1000  
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Scoring table: OLIGO\_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued\_Patents\_NA:\*

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SUMMARIES

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3	26	2.6	1618	6	PCT-US94-10358-3	Sequence 3, Appli
4	25	2.5	1610	6	PCT-US94-10358-7	Sequence 7, Appli
5	20	2.0	1634	1	US-07-816-283-1	Sequence 1, Appli
6	20	2.0	1265	1	US-07-816-283-3	Sequence 3, Appli
7	20	2.0	1452	1	US-08-149-093A-3	Sequence 3, Appli
8	20	2.0	1634	2	US-08-417-103-1	Sequence 1, Appli
9	20	2.0	1265	2	US-08-417-103-3	Sequence 3, Appli
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17	18	1.8	2238	1	US-07-841-651-1	Sequence 1, Appli
18	18	1.8	1296	1	US-07-816-283-9	Sequence 9, Appli
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23	17	1.7	489	1	US-07-879-685B-3	Sequence 3, Appli
24	17	1.7	722	2	US-08-702-344-8	Sequence 8, Appli
25	17	1.7	11725	3	US-08-756-506-1	Sequence 1, Appli
26	17	1.7	1498	4	US-08-775-428-1	Sequence 5, Appli
27	16	1.6	1351	1	US-07-816-283-5	Sequence 11, Appli
28	16	1.6	1796	1	US-07-816-283-11	Sequence 7, Appli
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34	16	1.6	1733	2	US-08-706-292-1	Sequence 1, Appli
35	16	1.6	959	2	US-08-634-331-1	Sequence 1, Appli
36	16	1.6	1899	2	US-08-634-331-2	Sequence 2, Appli
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39	16	1.6	1147	2	US-08-417-103-15	Sequence 15, Appli
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43	16	1.6	6143	2	US-08-612-521-3	Sequence 3, Appli
44	16	1.6	3505	3	US-08-376-843-43	Sequence 43, Appli
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ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/08411859  
; Patent No. 5985600  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, CHRISTOPHER J.  
; APPLICANT: KEITH JR., DUANE E.  
; APPLICANT: EDWARDS, ROBERT H.  
; TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID  
; TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED  
; TITLE OF INVENTION: PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
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; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/929,200  
; FILING DATE: 13-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LITHGOW, TIMOTHY J.  
; REGISTRATION NUMBER: 36,856  
; REFERENCE/DOCKET NUMBER: 22000-20526.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1829 base pairs  
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; TOPOLOGY: linear  
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 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P. O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77210  
 ; COMPUTER READABLE FORM:  
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 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/120.601  
 ; FILING DATE: 13 SEPTEMBER 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WILSON, MARK B.  
 ; REGISTRATION NUMBER: 37,259  
 ; REFERENCE/DOCKET NUMBER: INDA005P--  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (512) 418-3000  
 ; TELEFAX: (713) 789-2679  
 ; TELEX: 79-0924  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
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 ; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P. O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas

; COUNTRY: USA  
 ; ZIP: 77210  
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 ; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
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 ; FILING DATE: Concurrently herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/120.601  
 ; FILING DATE: 13 SEPTEMBER 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WILSON, MARK B.  
 ; REGISTRATION NUMBER: 37,259  
 ; REFERENCE/DOCKET NUMBER: INDA005P--  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (512) 418-3000  
 ; TELEFAX: (713) 789-2679  
 ; TELEX: 79-0924  
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 ; APPLICANT:  
 ; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P. O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77210  
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 ; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25  
 ; CURRENT APPLICATION DATA:  
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 ; FILING DATE: Concurrently herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/120.601  
 ; FILING DATE: 13 SEPTEMBER 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WILSON, MARK B.  
 ; REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: INDA005P--  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1610 base pairs  
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PCT-US94-10358-7

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5  
US-07-816-283-1  
Sequence 1, Application US/07816283  
Patent No. 5436155  
GENERAL INFORMATION:  
APPLICANT: Bell, Graeme I.  
APPLICANT: Yamada, Yuichiro  
APPLICANT: Seino, Susumu  
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: PO Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/816,283  
FILING DATE: 19911231  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1634 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-07-816-283-1

Query Match 2.0%; Score 20; DB 1; Length 1634;  
Best Local Similarity 100.0%; Pred. No. 0.73;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6  
US-07-816-283-3  
Sequence 3, Application US/07816283  
Patent No. 5436155  
GENERAL INFORMATION:  
APPLICANT: Bell, Graeme I.  
APPLICANT: Yamada, Yuichiro  
APPLICANT: Seino, Susumu  
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: PO Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/816,283  
FILING DATE: 19911231  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1265 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-07-816-283-3

Query Match 2.0%; Score 20; DB 1; Length 1265;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 CAACATGTTCCAGCATCT 282  
|||||  
DB 504 CAACATGTTCCAGCATCT 523

RESULT 7  
US-08-149-093A-3  
Sequence 3, Application US/08149093A  
Patent No. 5658783  
GENERAL INFORMATION:  
APPLICANT: Bunzow, James R  
APPLICANT: Grandy, David K  
TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific  
TITLE OF INVENTION: Opioid Receptor Gene and Uses  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,093A
; FILING DATE: 06-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5658783nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
;
US-08-149-093A-3

```

Query Match 2.0%; Score 20; DB 1; Length 1452;  
 Best Local Similarity 100.0%; Pred. No. 0.72;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 123 ACCAACATTTACATATTAA 142
Db 428 ACCAACATTTACATATTAA 447

```

```

RESULT 8
US-08-417-103-1
; Sequence 1, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,103
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,283
; FILING DATE: 01-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.

```

```

; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 100..1272
;
US-08-417-103-1

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Query Match 2.0%; Score 20; DB 2; Length 1634;  
 Best Local Similarity 100.0%; Pred. No. 0.73;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 263 CAACATGTTCAACGACATCT 282
Db 516 CAACATGTTCAACGACATCT 535

```

```

RESULT 9
US-08-417-103-3
; Sequence 3, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,103
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,283
; FILING DATE: 01-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1265 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..1260
;
US-08-417-103-3

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Query Match 2.0%; Score 20; DB 2; Length 1265;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 CAACATGTTCCACGCACT 282  
|||||  
Db 504 CAACATGTTCCACGCACT 523

## RESULT 10

US-08-417-103-13  
; Sequence 13, Application US/08417103  
; Patent No. 5723299  
; GENERAL INFORMATION:  
; APPLICANT: Bell, Graeme I.  
; APPLICANT: Yamada, Yuichiro  
; APPLICANT: Seino, Susumu  
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/417,103  
; FILING DATE: 05-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/816,283  
; FILING DATE: 01-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: ARCD:144  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1205 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 15..1187

## US-08-417-103-13

Query Match 2.0%; Score 20; DB 2; Length 1205;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 CAACATGTTCCACGCACT 282  
|||||  
Db 431 CAACATGTTCCACGCACT 450

## RESULT 11

US-08-147-949A-1  
; Sequence 1, Application US/08147949A  
; Patent No. 5747279  
; GENERAL INFORMATION:  
; APPLICANT: Pasternak, Gavril W.

; APPLICANT: Pan, Ying-Xian  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING  
; TITLE OF INVENTION: KAPPA3 OPIOID RECEPTORS, RECEPTORS  
; TITLE OF INVENTION: ENCODED THEREBY, AND USES THEREOF  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,949A  
; FILING DATE: 05-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 44782/JPW/JKM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; TELEX: 422523 COOP UI  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2600 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: N  
; ANTI-SENSE: N  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 299..1401  
; OTHER INFORMATION:  
; US-08-147-949A-1

Query Match 2.0%; Score 20; DB 2; Length 2600;  
Best Local Similarity 100.0%; Pred. No. 0.74;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 ACCAACATTTACATATTAA 142  
|||||  
Db 545 ACCAACATTTACATATTAA 564

## RESULT 12

US-08-911-245-3  
; Sequence 3, Application US/08911245  
; Patent No. 5821067  
; GENERAL INFORMATION:  
; APPLICANT: Bunzow, James R  
; APPLICANT: Grandy, David K  
; TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific  
; TITLE OF INVENTION: Opioid Receptor Gene and Uses  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Allegretti, Ltd.  
; STREET: 10 South Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,245
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149093
; FILING DATE: 06-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5821067nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
US-08-911-245-3
```

```
Query Match 2.0%; Score 20; DB 2; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 123 ACCAACATTTACATATTTAA 142
|||||
Db 428 ACCAACATTTACATATTTAA 447
```

```
RESULT 13
US-08-553-058C-3
; Sequence 3, Application US/08553058C
; Patent No. 5821219
; GENERAL INFORMATION:
; APPLICANT: Grisel, Judith E.
; APPLICANT: Grandy, David K.
; APPLICANT: Mogil, Jeffrey S.
; TITLE OF INVENTION: Opioid Antagonists and Methods of Their Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston LLP
; STREET: 121 S.W. Salmon, Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Version WP6, ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,058C
; FILING DATE: 11/3/95
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
```

```
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William D. No. 5821219nan, M.D.
; REGISTRATION NUMBER: 30,878
; REFERENCE/DOCKET NUMBER: 899-40006/WDN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
US-08-553-058C-3
```

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Query Match 2.0%; Score 20; DB 2; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 123 ACCAACATTTACATATTTAA 142
|||||
Db 428 ACCAACATTTACATATTTAA 447
```

```
RESULT 14
US-08-514-451A-3
; Sequence 3, Application US/08514451A
; Patent No. 5837809
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R.
; APPLICANT: Grandy, David K.
; APPLICANT: Civelli, Olivier
; APPLICANT: Reinscheid, Rainer K.
; APPLICANT: No. 5837809hacker, Hans-Peter
; APPLICANT: Monsma, Frederick J.
; TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID
; TITLE OF INVENTION: RECEPTOR LIGAND AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell
; ADDRESSEE: Leigh & Whinston LLP
; STREET: 121 S.W. Salmon, Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WP5.1 ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,451A
; FILING DATE: 08/11/95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/553,058
; FILING DATE: 11/13/95
; ATTORNEY/AGENT INFORMATION:
; NAME: William D. No. 5837809nan, M.D.
```

```
; REGISTRATION NUMBER: 30,878
; REFERENCE/DOCKET NUMBER: 899-45995/WDN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: cdna
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
US-08-514-451A-3
```

```
Query Match 2.0%; Score 20; DB 3; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 123 ACCAACATTTACATATTAA 142
|||||
Db 428 ACCAACATTTACATATTAA 447
```

```
RESULT 15
US-08-454-549-1
; Sequence 1, Application US/08454549
; Patent No. 5866324
; GENERAL INFORMATION:
; APPLICANT: EPPLER, C. Mark
; APPLICANT: OZENBERGER, Bradley A.
; APPLICANT: HULMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,549
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/1A818-US5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2706 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; TISSUE TYPE: Rat brain
US-08-454-549-1

Query Match 2.0%; Score 20; DB 3; Length 2706;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 123 ACCAACATTTACATATTAA 142
|||||
Db 353 ACCAACATTTACATATTAA 372
```

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Search completed: February 17, 2000, 10:12:07
Job time: 1922 sec
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GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.  
  
OM nucleic - nucleic search, using sw model  
  
Run on: February 17, 2000, 09:50:15 ; Search time 771.69 Seconds  
(without alignments)  
4892.721 Million cell updates/sec  
  
Title: US-08-455-683-11  
Perfect score: 1000  
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Scoring table: OLIGO\_NUC  
  
Searched: 4538634 seqs, 1887831982 residues  
  
Database : ESI:\*  
  
Word size : 0  
  
Number of hits that pass the threshold : 9077268

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2: em\_est2:\*  
3: em\_est3:\*  
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102: gb\_gss12:\*  
103: gb\_gss13:\*  
104: gb\_gss14:\*  
105: gb\_gss15:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	7.8	153	22	R31984
2	33	3.3	183	22	R81583
C 3	20	2.0	659	63	AI980732
4	19	1.9	415	20	M75869
C 5	19	1.9	360	24	D75109
6	19	1.9	206	31	AA317847
7	19	1.9	521	33	AA447244

R31984 yb62c10.r1  
R81583 yj04b04.r1  
AI980732 pat.pk003  
M75869 CEL06A11 Ch  
D75109 CELK096D7F  
AA317847 EST19840  
AA447244 zw93c04.r

8	19	1.9	443	41	AI056367	oy48c06.x
9	19	1.9	523	47	AI524239	th11d11.x
10	19	1.9	233	48	AI559367	tn21b12.x
11	19	1.9	679	50	AI679822	tu66b12.x
12	19	1.9	378	62	AV192296	AV192296
13	19	1.9	523	63	AI950015	wq15f02.x
14	19	1.9	161	71	AV312772	AV312772
15	19	1.9	683	74	AW176530	CM4-CT004
16	19	1.9	525	74	AW180364	MgA0474f
17	19	1.9	360	81	B50520	CIT-HSP-459
18	19	1.9	555	82	AQ735467	HS_3033_B
19	19	1.9	153	82	AQ736774	HS_3223_A
20	19	1.9	538	90	AQ039966	CIT-HSP-2
21	19	1.9	502	99	AQ241175	RPCI11-66
22	19	1.9	389	100	AQ270199	HS_2037_A
23	19	1.9	232	100	AQ281671	RPCI11-89
24	19	1.9	508	100	AQ283756	RPCI11-91
25	19	1.9	354	105	AQ604009	HS_2136_A
26	19	1.9	528	105	AQ610369	HS_5105_A
27	18	1.8	367	20	T01065	WEST01786 E
28	18	1.8	187	20	Z20996	HSAAADHZ B
29	18	1.8	466	21	R15256	yf89d03.r1
30	18	1.8	447	21	T94320	ye37h04.s1
31	18	1.8	224	24	H74768	313 Deletio
32	18	1.8	532	25	N96144	21840 Lambd
33	18	1.8	253	25	N97156	22335 Lambd
34	18	1.8	440	26	W76111	zd65c03.r1
35	18	1.8	427	31	AA282414	zs90b03.r
36	18	1.8	316	31	AA296456	EST11038
37	18	1.8	261	32	AA331167	EST35211
38	18	1.8	337	32	AA361360	EST70628
39	18	1.8	512	33	AA393081	zt69a10.r
40	18	1.8	332	33	AA412109	zt69a10.s
41	18	1.8	300	35	C59880	C59880 Yuji
42	18	1.8	308	37	AA679697	ah13d02.s
43	18	1.8	532	38	AA749488	L30-29M13
44	18	1.8	512	38	AA753659	97BS0143
45	18	1.8	583	39	C85539	C85539 Mous

ALIGNMENTS

RESULT	1	R31984	153 bp	mRNA	EST	28-APR-1995
LOCUS		Yh62c10.r1	Soares placenta Nb2HP	Homo sapiens	cdna clone	
DEFINITION		IMAGE:134322 5' similar to gb:L25119 MU-TYPE OPIOID RECEPTOR (HUMAN);, mRNA sequence.				
ACCESSION		R31984				
VERSION		R31984.1	GI:787827			
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS		1 (bases 1 to 153)				
		Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.				
TITLE		The WashU-Merck EST Project				
JOURNAL		Unpublished (1995)				
COMMENT		Contact: Wilson RK				
		Washington University School of Medicine				
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
		Tel: 314 286 1800				
		Fax: 314 286 1810				
		Email: est@watson.wustl.edu				
		Insert Size: 947				
		High quality sequence stops: 120				
		Source: IMAGE Consortium, LLNL				

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 947 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 120.

FEATURES  
source  
1. .153  
/organism="Homo sapiens"  
/db\_xref="GDB:540134"  
/db\_xref="taxon:9606"  
/clone="IMAGE:134322"  
/clone\_lib="Soares placenta Nb2HP"  
/sex="Female"  
/dev\_stage="placenta obtained at birth (full term)"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTCGGCGCCGACGAATTTTTCCTGCTGCTACACCTGA 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

BASE COUNT 25 a 49 c 37 g 42 t  
ORIGIN  
Query Match 7.8%; Score 78; DB 22; Length 153;  
Best Local Similarity 100.0%; Pred. NO. 4.6e-30;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 529 GCGTCTTCATCTTTGCCCTCGTGATCCCTGTCCCTCATCATCGTCTGCTACACCTGA 588  
|||||  
Db 1 GCGTCTTCATCTTTGCCCTCGTGATCCCTGTCCCTCATCATCGTCTGCTACACCTGA 60  
QY 589 TGATCCTCGGTCTCAAGA 606  
|||||  
Db 61 TGATCCTCGGTCTCAAGA 78

RESULT 2  
R81583  
LOCUS R81583 183 bp mRNA EST 12-JUN-1995  
DEFINITION YJ04b04.r1 Soares placenta Nb2HP Homo sapiens cdna clone  
IMAGE:147727 5' similar to gb:L25119 MU-TYPE OPIOID RECEPTOR (HUMAN);, mRNA sequence.

ACCESSION R81583  
VERSION R81583.1 GI:858186  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 183)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)

COMMENT On May 8, 1995 this sequence version replaced gi:800395.  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 1518  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert length: 1518 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 1.

FEATURES

source  
Location/Qualifiers  
1. .183  
/organism="Homo sapiens"  
/db\_xref="GDB:559413"  
/db\_xref="taxon:9606"  
/clone="IMAGE:147727"  
/clone\_lib="Soares placenta Nb2Hp"  
/sex="Female"  
/dev\_stage="placenta obtained at birth (full term)"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: placenta; vector: pT7T3D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAGAAATCGCGCGCAGGAATTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

BASE COUNT 31 a 56 c 40 g 46 t 10 others  
ORIGIN

Query Match 3.3%; Score 33; DB 22; Length 183;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 CAACCTGCGTAGGATCACCAGACTGGTCCTGGT 676  
|||||  
Db 109 CAACCTGCGTAGGATCACCAGACTGGTCCTGGT 141

RESULT 3  
AI980732/c  
LOCUS  
DEFINITION  
pat.pk0032.b12.f chicken activated T cell cDNA Gallus gallus cDNA clone pat.pk0032.b12.f 5' similar to U1 snRNP 70K protein, mRNA sequence.

AI980732 659 bp mRNA EST 15-SEP-1999  
AI980732  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
chicken.  
Gallus gallus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
An expressed-sequence-tag database of activated chicken T cells: sequence analysis of 5596 clones  
Unpublished (1999)  
On Dec 20, 1995 this sequence version replaced gi:1130941.  
Contact: Joan Burnside  
Molecular Endocrinology  
University of Delaware  
40 Townsend Hall, Newark, DE 19717, USA  
Tel: 302 831-1345  
Fax: 302 831-3651  
Email: joan@udel.edu  
Seq primer: T7.

FEATURES  
source  
Location/Qualifiers  
1. .659  
/organism="Gallus gallus"  
/db\_xref="taxon:9031"  
/clone="pat.pk0032.b12.f"  
/clone\_lib="chicken activated T cell cDNA"  
/sex="male"  
/cell\_type="Con A-activated splenic T cell"

/lab\_host="E.coli IOP10 F"  
/note="Vector: pCDNA3"  
BASE COUNT 215 a 130 c 165 g 137 t 12 others  
ORIGIN

Query Match 2.0%; Score 20; DB 63; Length 659;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 560 CCTCATCATCATCGTCTGCT 579  
|||||  
Db 63 CCTCATCATCATCGTCTGCT 44

RESULT 4  
M75869  
LOCUS  
DEFINITION  
M75869 415 bp mRNA EST 16-SEP-1992  
CEL06A11 Chris Martin sorted cDNA library Caenorhabditis elegans cDNA clone cm06a11 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
M75869.1 GI:275214  
EST.  
Caenorhabditis elegans.  
Caenorhabditis elegans

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT  
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 415)  
Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A., Hillier,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N., Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J. and Sulston,J.  
A survey of expressed genes in Caenorhabditis elegans  
Nature Genet. 1, 114-123 (1992)  
93250982  
Contact: Waterston R.H.(USA) and Sulston J.E.(UK)  
(USA) Dept. of Genetics or (UK)  
(USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of Molecular Biology  
Box 8232,4566 Scott Ave.,St. Louis,MI 63110,USA,or,Hills Road,Cambridge CB2 2QH,UK  
Tel: (USA) (314)3627072 or (UK) (0223)248011  
Fax: (USA) (314)3624137 or (UK) (0223)402008  
Email: rwe@nematode.wustl.edu or jes@mrc-lmba.cambridge.ac.uk  
single read.

FEATURES  
source  
Location/Qualifiers  
1. .415  
/organism="Caenorhabditis elegans"  
/strain="Bristol N2"  
/db\_xref="taxon:6239"  
/clone="cm06a11"  
/clone\_lib="Chris Martin sorted cDNA library"  
/lab\_host="MC1061"  
/note="Vector: lambda phage SHLX2; Mixed stage hermaphrodite cDNA library. Partially normalized by successively picking groups of clones that didn't hybridize to previously picked clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)) Host: MC1061"

BASE COUNT 123 a 69 c 95 g 125 t 3 others  
ORIGIN

Query Match 1.9%; Score 19; DB 20; Length 415;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 560 CCTCATCATCATCGTCTGC 578  
|||||  
Db 78 CCTCATCATCATCGTCTGC 96

RESULT 5

D75109/c  
LOCUS D75109 360 bp mRNA EST 18-OCT-1999  
DEFINITION CELK096D7F Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans CDNA clone yk96d7 5', mRNA sequence.  
ACCESSION D75109  
VERSION D75109.1 GI:1120893  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 360)  
AUTHORS Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and Tabara,H.  
TITLE Toward an expression map of the C.elegans genome  
JOURNAL Unpublished (1994)  
COMMENT Contact: Yuji Kohara  
Gene Library Lab  
National Institute of Genetics  
Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp  
High quality sequence stop: 322.  
FEATURES  
source Location/Qualifiers  
1..360  
/organism="Caenorhabditis elegans"  
/strain="N2"  
/db\_xref="taxon:6239"  
/clone="yk96d7"  
/clone\_lib="Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"  
/sex="hermaphrodite"  
/dev\_stage="embryo"  
BASE COUNT 98 a 120 c 64 g 74 t 4 others  
ORIGIN  
Query Match 1.9%; Score 19; DB 24; Length 360;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 666 CTGGTCCTGGTGGTGGTGG 684  
Db 173 CTGGTCCTGGTGGTGGTGG 155  
RESULT 6  
AA317847  
LOCUS AA317847 206 bp mRNA EST 19-APR-1997  
DEFINITION EST19840 Retina II Homo sapiens CDNA 5' end, mRNA sequence.  
ACCESSION AA317847  
VERSION AA317847.1 GI:1970173  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 206)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,I.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,

Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.  
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
MEDLINE 12140200  
COMMENT On Sep 12, 1996 this sequence version replaced gi:1402207.  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.  
FEATURES  
source Location/Qualifiers  
1..206  
/organism="Homo sapiens"  
/db\_xref="ATCC (inhost):118310"  
/db\_xref="taxon:9606"  
/clone\_lib="Retina II"  
/sex="mixed"  
/dev\_stage="adult"  
/note="Organ: retina; Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"  
BASE COUNT 50 a 48 c 65 g 41 t 2 others  
ORIGIN  
Query Match 1.9%; Score 19; DB 31; Length 206;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 725 CCTGGTGGAGGCTCTGGGG 743  
Db 48 CCTGGTGGAGGCTCTGGGG 66  
RESULT 7  
AA447244  
LOCUS AA447244 521 bp mRNA EST 03-JUN-1997  
DEFINITION ZW93c04.r1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens CDNA clone IMAGE:784518 5', mRNA sequence.  
ACCESSION AA447244  
VERSION AA447244.1 GI:2159909  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 521)  
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.  
WashU-Merck EST Project 1997  
Unpublished (1997)  
On Apr 14, 1993 this sequence version replaced gi:692829.  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 490.  
FEATURES  
Location/Qualifiers

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source 1. .521
/organism="Homo sapiens"
/db_xref="GDB:5982136"
/db_xref="taxon:9606"
/clone="IMAGE:784518"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGIGGAGCGCGCTTAATTTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 142 a 128 c 127 g 124 t
ORIGIN

Query Match 1.9%; Score 19; DB 33; Length 521;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 725 CCTGGTGGAGGCTCTGGGG 743
|||||
Db 498 CCTGGTGGAGGCTCTGGGG 516

RESULT 8
AI056367 443 bp mRNA EST 24-SEP-1998
LOCUS oy48c06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1669066 3',
DEFINITION mRNA sequence.
ACCESSION AI056367
VERSION AI056367.1 GI:3330233
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 443)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGA), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1404573.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 593 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
1. .443
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1669066"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"

FEATURES
source
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/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGIGGAGCGCGCATATCTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 86 a 106 c 119 g 132 t
ORIGIN

Query Match 1.9%; Score 19; DB 41; Length 443;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 GGCACCAAAGTCAGGGAAG 453
|||||
Db 152 GGCACCAAAGTCAGGGAAG 170

RESULT 9
AI524239 523 bp mRNA EST 18-MAR-1999
LOCUS th11d11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2117973 3',
DEFINITION mRNA sequence.
ACCESSION AI524239
VERSION AI524239.1 GI:4438374
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 523)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jul 29, 1997 this sequence version replaced gi:2285735.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco
High quality sequence stop: 434.
Location/Qualifiers
1. .523
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2117973"
/clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATTCCTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 167 a 89 c 91 g 174 t
ORIGIN
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Query Match 1.9%; Score 19; DB 47; Length 523;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 GGAATGCTATGTTTCTT 91  
|||||  
Db 74 GGAATGCTATGTTTCTT 92

RESULT 10  
AI559367 233 bp mRNA EST 12-MAY-1999  
LOCUS tn21b12.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2168255 3',  
DEFINITION mRNA sequence.  
ACCESSION AI559367  
VERSION AI559367.1 GI:4509572  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 233)  
AUTHORS NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index  
JOURNAL Unpublished (1998)  
COMMENT On Jun 5, 1998 this sequence version replaced gi:3189024.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 568 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 224  
POLYA=No.

FEATURES Location/Qualifiers  
source 1..233  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2168255"  
/clone\_lib="NCI\_CGAP\_Brn25"  
/tissue\_type="anaplastic oligodendroglioma"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTCAAGTGGGAGCGCGCATAGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."  
BASE COUNT 53 a 46 c 53 g 81 t  
ORIGIN

Query Match 1.9%; Score 19; DB 48; Length 233;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 GGCACCAAGTCAGGGAAG 453

Db 128 GGCACCAAGTCAGGGAAG 146  
|||||

RESULT 11  
AI679822/c  
LOCUS AI679822  
DEFINITION tu66b12.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2255999 3',  
similar to TR:000112 000112 LIVER-SPECIFIC BHLH-ZIP TRANSCRIPTION FACTOR 1, mRNA sequence.  
ACCESSION AI679822  
VERSION AI679822.1 GI:4890004  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 679)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT On Dec 20, 1995 this sequence version replaced gi:1131236.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco  
High quality sequence stop: 397.  
FEATURES Location/Qualifiers  
source 1..679  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2255999"  
/clone\_lib="NCI\_CGAP\_Gas4"  
/tissue\_type="poorly differentiated adenocarcinoma with signet ring cell features"  
/lab\_host="DH10B"  
/note="Organ: stomach; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

BASE COUNT 102 a 207 c 207 g 163 t  
ORIGIN

Query Match 1.9%; Score 19; DB 50; Length 679;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 433 GAGGCACCAAGTCAGGGA 451  
|||||  
Db 569 GAGGCACCAAGTCAGGGA 551

RESULT 12  
AV192296  
LOCUS AV192296 378 bp mRNA EST 22-JUL-1999  
DEFINITION AV192296 Yuji Kohara unpublished cDNA:Strain N2 hermaprodite embryo Caenorhabditis elegans cDNA clone yk603f8 5', mRNA sequence.  
ACCESSION AV192296  
VERSION AV192296.1 GI:5574448  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 378)  
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.

Expressed genes in C.elegans  
Unpublished (1999)  
On Jun 22, 1998 this sequence version replaced gi:3247111.  
Contact: Yuji Kohara  
Gene Library Lab  
National Institute of Genetics  
Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp.

FEATURES  
source  
1..378  
/organism="Caenorhabditis elegans"  
/strain="N2"  
/db\_xref="taxon:6239"  
/clone="yk603f8"  
/clone\_lib="Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"  
/sex="hermaphrodite"  
/dev\_stage="embryo"  
Location/Qualifiers  
112 a 65 c 87 g 113 t 1 others  
BASE COUNT  
ORIGIN

Query Match 1.9%; Score 19; DB 62; Length 378;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 560 CCTCATCATCATCGTCTGC 578  
|||||  
Db 59 CCTCATCATCATCGTCTGC 77

RESULT 13  
AI950015 523 bp mRNA EST 06-SEP-1999  
LOCUS  
DEFINITION Wq15f02.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2471355 3' similar to WP:126E3.3 CE14188 PDZ DOMAIN ;, mRNA sequence.  
AI950015  
ACCESSION AI950015.1 GI:5742325  
VERSION  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 523)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
On Jun 22, 1998 this sequence version replaced gi:3248182.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Seq primer: -40UP from Gibco  
High quality sequence stop: 458.  
Location/Qualifiers

source  
1..523  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2471355"  
/clone\_lib="NCI\_CGAP\_Kid12"  
/tissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP\_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."   
BASE COUNT 133 a 124 c 137 g 129 t  
ORIGIN

Query Match 1.9%; Score 19; DB 63; Length 523;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 255 GATTACTACAACATGTTCA 273  
|||||  
Db 257 GATTACTACAACATGTTCA 275

RESULT 14  
AV312772/c 161 bp mRNA EST 08-NOV-1999  
LOCUS  
DEFINITION AV312772 RIKEN full-length enriched, adult male thymus Mus musculus cDNA clone 5830405G21 3', mRNA sequence.  
AV312772  
ACCESSION AV312772.1 GI:6278024  
VERSION  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 161)  
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al.)  
Unpublished (1999)  
On Jun 22, 1998 this sequence version replaced gi:3247418.  
Contact: Yoshihide Hayashizaki  
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory  
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: -81-298-36-9013  
Fax: +81-298-36-9098  
Email: genome-res@rtc.riken.go.jp,  
URL:<http://genome.rtc.riken.go.jp/>  
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
Itoh,M., Kitsu nai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,

Okazaki,Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

FEATURES  
source  
Location/Qualifiers  
1. .161  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="5830405G21"  
/clone\_lib="RIKEN full-length enriched, adult male thymus"  
/sex="male"  
/tissue\_type="thymus"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Site\_1: Sali; Site\_2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTCTTTVN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 10.0 and subtraction to Rot = 100.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGAGAGATTCTCGAGTTAATTAATTAATCCCCCCCCC  
3']. cDNA was cloned into the XhoI and BamHI sites.  
vector: a modified pbluescript KS(+) after bulk excision  
from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end:  
BamHI."

BASE COUNT 48 a 32 c 20 g 61 t  
ORIGIN

Query Match 1.9%; Score 19; DB 71; Length 161;  
Best Local Similarity 100.0%; Pred.No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 CCTTGAAGGCCAAGATCAT 376  
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Db 161 CCTTGAAGGCCAAGATCAT 143

RESULT 15  
AW176530/c  
LOCUS AW176530 683 bp mRNA EST 16-NOV-1999  
DEFINITION CM4-CT0041-270899-009-a06 CT0041 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW176530  
VERSION AW176530.1 GI:6442567  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 683)  
AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.  
TITLE The FAPESP/LICR Human Cancer Genome Project  
JOURNAL Unpublished (1999)  
COMMENT On May 18, 1998 this sequence version replaced gi:3137999.  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CT0041-270899-009-a06&t3=1999-08-27&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence start: 53  
High quality sequence stop: 662.

FEATURES  
source  
Location/Qualifiers  
1. .683  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CT0041"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: pUC18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application NO.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

BASE COUNT 156 a 202 c 140 g 182 t 3 others  
ORIGIN

Query Match 1.9%; Score 19; DB 74; Length 683;  
Best Local Similarity 100.0%; Pred.No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

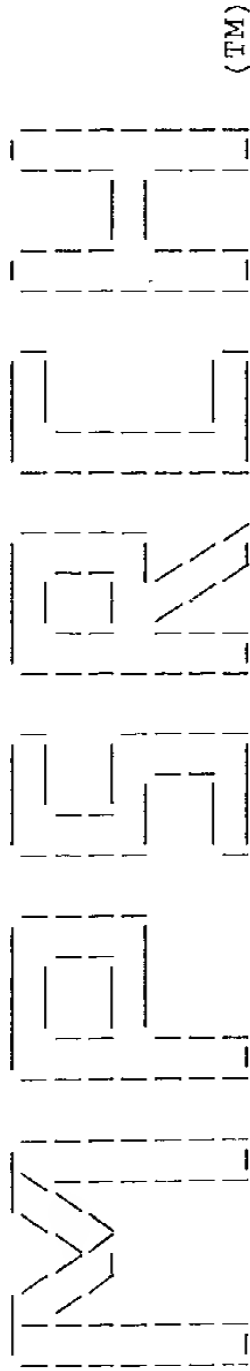
QY 725 CCTGGTGGAGGCTCTGGGG 743  
|||||  
Db 480 CCTGGTGGAGGCTCTGGGG 462

Search completed: February 17, 2000, 09:50:20  
Job time: 795 sec



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Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 17 11:14:53 2000; MasPar time 19.73 Seconds  
318.037 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-455-683-12  
Description: (1-295) from US08455683.pep  
Perfect Score: 2229  
Sequence: 1 YTKMKTATNIYIFNLALADA.....NTVQDPAYLREIDGMNKPV 295

Scoring table: PAM 150  
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq35  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39

Statistics: Mean 33.708; Variance 153.726; scale 0.219

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2223	99.7	295	12	R67672 Human kappa opioid re	3.49e-193
2	2192	98.3	380	27	W30297 Human kappa opioid re	2.86e-190
3	2192	98.3	380	17	R88722 Human kappa opioid re	2.86e-190
4	2192	98.3	427	27	W30298 Human kappa opioid re	2.86e-190
5	2136	95.8	380	34	W44939 Mouse kappa opiate re	5.22e-185
6	2136	95.8	380	13	R67669 Mouse kappa opioid re	5.22e-185
7	2132	95.6	380	14	R72591 Mammalian kappa opioi	1.24e-184
8	2132	95.6	380	14	R76783 Rat kappa opiate rece	1.24e-184
9	2008	90.1	424	27	W30299 Human kappa opioid re	5.44e-173
10	1524	68.4	398	34	W44937 Mouse mu opiate recep	1.16e-127
11	1522	68.3	356	11	R65188 Murine mu-subtype opi	1.78e-127
12	1522	68.3	398	14	R76781 Rat mu opiate recepto	1.78e-127
13	1522	68.3	400	13	R71966 Human mu opioid recep	1.78e-127
14	1520	68.2	398	13	R71964 Rat mu opioid recepto	2.73e-127
15	1520	68.2	400	14	R76780 Human mu opiate recep	2.73e-127
16	1452	65.1	372	14	R76782 Rat delta opiate rece	6.10e-121

17	1448	65.0	372	9	R48629	Sequence of murine de	1.44e-120
18	1448	65.0	372	13	R67670	Mouse delta opioid re	1.44e-120
19	1448	65.0	372	34	W44938	Mouse delta opiate re	1.44e-120
20	1348	60.5	371	10	R66503	Murine delta opioid r	3.05e-111
21	1345	60.3	367	13	R71968	Rat opioid receptor.	5.80e-111
22	1343	60.3	367	13	R67671	Mouse opioid receptor	8.90e-111
23	1336	59.9	367	14	R76638	Rat opiorph receptor	4.00e-110
24	1335	59.9	367	25	W26582	Rat methadone-specifi	4.95e-110
25	1335	59.9	367	36	W80549	Rat methadone-specifi	4.95e-110
26	1335	59.9	367	24	W25217	Rat orphanin FQ recep	4.95e-110
27	1066	47.8	367	13	R74298	Mouse kappa-3 opioid	4.89e-85
28	830	37.2	391	7	R39259	Human somatostatin re	2.96e-63
29	830	37.2	391	7	R39260	Murine somatostatin r	2.96e-63
30	785	35.2	369	7	R39262	Murine somatostatin r	4.01e-59
31	780	35.0	369	7	R39261	Human somatostatin re	1.15e-58
32	780	35.0	369	19	R97269	Human somatostatin re	1.15e-58
33	767	34.4	369	5	R27504	Pituitary somatostati	1.79e-57
34	736	33.0	333	13	R72985	Epsilon opioid recept	1.24e-54
35	727	32.6	322	16	R48754	Rat RGH G-protein cou	8.22e-54
36	727	32.6	322	19	W02726	Rat RGHJP G-protein c	8.22e-54
37	683	30.6	418	7	R39263	Human somatostatin re	8.57e-50
38	661	29.7	328	13	R72984	Epsilon opioid recept	8.66e-48
39	658	29.5	242	23	W10017	G-protein coupled rec	1.62e-47
40	599	26.9	428	7	R39264	Murine somatostatin r	3.72e-42
41	586	26.3	241	23	W10016	G-protein coupled rec	5.60e-41
42	545	24.5	349	18	R95070	Human galanin recepto	2.84e-37
43	545	24.5	349	14	R79443	Galanin receptor.	2.84e-37
44	522	23.4	372	25	W24561	Rat galanin receptor	3.35e-35
45	522	23.4	372	29	W40135	Rat GalR2 receptor pr	3.35e-35

ALIGNMENTS

RESULT 1	ID	R67672 standard; Protein; 295 AA.
AC	R67672;	
DT	18-AUG-1995	(first entry)
DE	Human kappa opioid receptor partial protein.	
KW	Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;	
KW	transmembrane domain; somatostatin; receptor; human; expression vector;	
KW	truncate; chimaeric; assay; probe.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	misc_difference 169	/label= Any amino acid
FT	misc_difference 181	/label= Any amino acid
FT	misc_difference 265	/label= Any amino acid
FT	misc_difference 269	/label= Any amino acid
PN	W09428132-A.	
PD	08-DEC-1994.	
PF	20-MAY-1994; U05747.	
PR	20-MAY-1993; US-066296.	
PR	30-JUL-1993; US-100694.	
PR	05-NOV-1993; US-147592.	
PA	(ARCH-) ARCH DEV CORP.	
PI	Bell GI, Reisine T, Yasuda K;	
DR	WPI: 95-022804/03.	
DR	N-PSDB; Q75931.	
PT	Polynucleotides and peptides derived from opioid receptor	
PT	polypeptides - for use in therapeutic compositions and in	
PT	screening assays for useful drug substances.	
PS	Claim 12; Page 236-239; 300pp; English.	
CC	The partial amino acid sequence of the novel human kappa opioid receptor.	
CC	The corresponding gene was isolated from a human brain hippocampus cDNA	
CC	library using a probe from the mouse kappa opioid receptor gene (Q75926).	
CC	The gene is missing the N-terminal sequence. The C-terminal sequence is	
CC	very similar to the mouse kappa opioid receptor sequence. Of the	
CC	C-terminal 293 amino acids, 281 residues are identical and 6 residues	
CC	have conservative substitutions. The gene encoding the human opioid	
CC	receptor can be placed in a suitable expression vector for production of	

CC the protein in a cell. The opiod receptors thus produced are useful for  
CC the development of novel assays designed to select or improve substances,  
CC capable of interacting with the opiod receptor proteins, for use in  
CC diagnosis, drug design and therapeutic applications.  
SQ Sequence 295 AA;

Query Match 99.7%; Score 2223; DB 12; Length 295;  
Best Local Similarity 99.7%; Pred. No. 3.49e-193;  
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 ytkmktatniyifnlaladalvtttmpfqstvylnmswpfgdvlcxivisidynnftsi 60  
QY 1 YTKMKTATNIYIFENLALADALVTTTMPFQSTVYLMNSWPFGDVLCXIVISIDYNNMFTSI 60  
Db 61 flltmsvdryiavchp vkaldfrt plkakiinicilwllsssvgisai vlggtkvregvd 120  
QY 61 FTLTMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLSSSVGISAIVLGGTKVREDVD 120  
Db 121 viecclqfpddyswdl fmkicvfifafvipvlliiivcytlmilrlkxvrl lsgsrek 180  
QY 121 VIECCLOFPDDDDYSWDLFMKICVFIFAFVIPVLLIIIVCYTLMILRLKXVRLLSGSREKD 180  
Db 181 xnlrritrlvlvvavfvvcwtpihifilvealgstshstaalssyfyfci algytnssl 240  
QY 181 XNLRRITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFYFCIALGYTNSSLN 240  
Db 241 pilyafl denfkrcfrcfplkxmmerxstsrvtntvqdpaylreidgm nkp 295  
QY 241 PILYAFLDENFKRCFRDCFPLKXMEXRSTSRVENTVQDPAYLREIDGMNKP 295

RESULT 2

ID W30297 standard; Protein; 380 AA.  
AC W30297;  
DT 14-APR-1998 (first entry)  
DE Human kappa opiod receptor.  
KW Selective target cell activation; G protein-coupled receptor;  
KW RASSL; gene therapy; cell proliferation; kappa opiod receptor;  
KW human; transgenic animal; arrhythmia; bone disease; seizure;  
KW vascular contraction; disease model.  
OS Homo sapiens.

FH Key Location/Qualifiers  
FT Domain 1..58  
FT /label= N-terminus  
FT /note= "extracellular"  
FT 59..85  
FT /label= TMH1  
FT /note= "transmembrane"  
FT 86..95  
FT /label= I1  
FT /note= "cytoplasmic"  
FT 96..117  
FT /label= TMH2  
FT /note= "transmembrane"  
FT 118..132  
FT /label= E2  
FT /note= "Extracellular"  
FT 133..154  
FT /label= TMH3  
FT /note= "transmembrane"  
FT 155..173  
FT /label= I2  
FT /note= "Cytoplasmic"  
FT 174..196  
FT /label= TMH4  
FT /note= "transmembrane"  
FT 197..222  
FT /label= E2  
FT /note= "extracellular"  
FT 223..247  
FT /label= TMH5  
FT /note= "transmembrane"  
FT 248..275

FT /label= I3  
FT /note= "Cytoplasmic"  
FT 276..299  
FT /label= TMH6  
FT /note= "Transmembrane"  
FT 300..311  
FT /label= E3  
FT /note= "Extracellular"  
FT 312..333  
FT /label= TMH7  
FT /note= "transmembrane"  
FT 334..380  
FT /label= C-terminus  
FT /note= "cytoplasmic"  
FT 131..210  
FT Modified\_site 25  
FT /note= "potential N-glycosylation"  
FT 39  
FT /note= "potential N-glycosylation"  
FT 345  
FT /note= "palmitate"  
PN WC9735478-A1.  
PD 02-OCT-1997.  
PF 25-MAR-1997; U05334.  
PR 26-MAR-1996; US-622348.  
PA (REGC ) UNIV CALIFORNIA.  
PI Conklin BR;  
DR WPI; 97-502739/46.  
DR N-PSDB; T90998.  
PT Selective activation of target cell expressing modified G protein  
PT coupled receptor - allows control of cellular proliferation,  
PT especially for amplification of transfected cells in gene therapy  
PS Example 1; Page 74-76; 117pp; English.  
CC This protein comprises human kappa opiod receptor (KOR), a  
CC G protein-coupled receptor implicated in neurotransmission. A  
CC novel method for selectively activating a target cell (TC)  
CC comprises: (i) introducing into the cell a nucleic acid sequence  
CC (I) that expresses a G protein-coupled receptor (A) modified to be  
CC activated superiorly by a synthetic ligand (RASSL); and (ii)  
CC exposing the transfected cell to small synthetic molecules (B) that  
CC bind to and activate (A), inducing the G protein coupled cellular  
CC response associated with receptor activation. (A) has: (a)  
CC decreased binding affinity for a selected natural ligand of the  
CC native receptor; (b) binding affinity for (B); and (c) is activated  
CC by binding (B) sufficiently to produce the required cellular  
CC response. Also new are: (1) transgenic cells including  
CC heterologous (I) in the genome; (2) cellular implants comprising a  
CC TC transfected with (I); (3) isolated (I); and (4) transgenic  
CC non-human animals expressing (A). Activation of (A) results, in  
CC vitro or in vivo, in cellular proliferation, or secretion of a  
CC cellular product, particularly a heterologous therapeutic protein  
CC encoded by a second inserted nucleic acid sequence. Particularly  
CC it is used to expand the relatively few cells that are successfully  
CC transfected during gene therapy procedures. Other responses that  
CC can be regulated are cell migration and contraction, or pigment  
CC production. In transgenic animals, expression or stimulation of  
CC (A) is designed to develop cardiac arrhythmia, symptoms of bone  
CC disease, seizures, vascular contractions, dementia, neurodegeneration  
CC etc., for use as models of these diseases (claimed). The transgenic  
CC animals are also used for production of improved food products  
CC (e.g. increased calcium content in eggshells or altered fat/lean  
CC ratios) or to control fertility or induce labour. A RASSL derived  
CC from KOR, designated RASSL OR1 (see W30299), was generated by  
CC mutation of the KOR cDNA sequence (see T90998).  
SQ Sequence 380 AA;

Query Match 98.3%; Score 2192; DB 27; Length 380;  
Best Local Similarity 97.6%; Pred. No. 2.86e-190;  
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvtttmpfqstvylnmswpfgdvlcxivisidynnftsi 146  
QY 1 YTKMKTATNIYIFENLALADALVTTTMPFQSTVYLMNSWPFGDVLCXIVISIDYNNMFTSI 60

Db	147	ftltmmsvdryiavchp vkaldfrt plkakiinicilwllsssvgisai vlggtkvredvd	206
QY	61	FTLTMSVDRIYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVD	120
Db	207	viectlqfpdddydwldfmkicvfifafvipvliiivcytlmilrlksvrlsgsrek	266
QY	121	VIECCLQFPDDDDYSWDLFMKICVFIFAFVIPVLIIVCYTLMILRLKXXVRLSSGREKD	180
Db	267	nlrritrlvlvvavfvvcwtpihifilvealgstshstaalssyyfci algytnssln	326
QY	181	XLNLRITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN	240
Db	327	pilyafldenfkrcfrdcfplkmmrqstsrvrntvqdpaylrdidgm-nkpv	380
QY	241	PILYAFLDENFKRCFRDFCFPLKMMXERXSTSRVRNTVQDPAYLREIDGMMNKPV	295
RESULT 3			
ID	R88722	standard; Protein; 380 AA.	
AC	R88722;		
DT	04-SEP-1996	(first entry)	
DE	Human kappa opioid receptor.		
KW	Human; kappa opioid receptor; psychiatric disorder; cardiovascular; neurology; diagnosis.		
KW	Homo sapiens.		
PN	WO9601898-A1.		
PD	25-JAN-1996.		
PF	07-JUL-1995; F00912.		
PR	11-JUL-1994; FR-008531.		
PA	(UYST-) UNIV PASTEUR STRASBOURG LOUIS.		
PI	Kieffer B, Simonin F;		
DR	WPI; 96-097628/10.		
DR	N-PSDB; T12550.		
PT	New nucleic acid encoding the human Kappa opioid receptor - useful in diagnosis and therapy, and for isolating receptor ligands and modulators		
PS	Claim 7; Page 13-15; 30pp; French.		
CC	The sequence coding for the human kappa opioid receptor was obtained from two overlapping cDNA fragments isolated from a human placental cDNA library. The fragments were amplified from the library using PCR primers based on the sequence of human genomic clones which hybridised with a murine delta receptor cDNA probe. Nucleotide probes derived from the kappa opioid receptor coding sequence are useful for diagnosis of neurological, cardiovascular and psychiatric disorders associated with opioid receptors. The receptor can be used for identifying e.g. agonists of its activity for potential use as analgesics.		
SQ	Sequence 380 AA;		
Query Match 98.3%; Score 2192; DB 17; Length 380;			
Best Local Similarity 97.6%; Pred. No. 2.85e-190;			
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;			
Db	87	ytkmktatniyifnlaladalvttmpfqstvylnmswpfgdvlckivisi dyymftsi	146
QY	1	YTKMKTAINIYIFNLALADALVTTMPFQSTVYLMNSWPFQDVLCKIVISIDYNNFTSI	60
Db	147	ftltmmsvdryiavchp vkaldfrt plkakiinicilwllsssvgisai vlggtkvredvd	206
QY	61	FTLTMSVDRIYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVD	120
Db	207	viectlqfpdddydwldfmkicvfifafvipvliiivcytlmilrlksvrlsgsrek	266
QY	121	VIECCLQFPDDDDYSWDLFMKICVFIFAFVIPVLIIVCYTLMILRLKXXVRLSSGREKD	180
Db	267	nlrritrlvlvvavfvvcwtpihifilvealgstshstaalssyyfci algytnssln	326
QY	181	XLNLRITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN	240
Db	327	pilyafldenfkrcfrdcfplkmmrqstsrvrntvqdpaylrdidgm-nkpv	380
QY	241	PILYAFLDENFKRCFRDFCFPLKMMXERXSTSRVRNTVQDPAYLREIDGMMNKPV	295

RESULT 4			
ID	W30298	standard; Protein; 427 AA.	
AC	W30298;		
DT	14-APR-1998	(first entry)	
DE	Human kappa opioid receptor fusion polypeptide.		
KW	Selective target cell activation; G protein-coupled receptor; RASSL; gene therapy; cell proliferation; kappa opioid receptor; human; transgenic animal; arrhythmia; bone disease; seizure; vascular contraction; disease model.		
OS	Chimeric - Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..30	/label= Sig_peptide
FT			/note= "prolactin signal sequence"
FT	Peptide	31..38	
FT	Protein	/label= FLAG	
FT		39..417	
FT		/label= KOR	
FT	Domain	/note= "human kappa opioid receptor"	
FT		39..95	
FT		/label= N-terminus	
FT		/note= "extracellular"	
FT	Domain	96..122	
FT		/label= TMH1	
FT		/note= "transmembrane"	
FT	Domain	123..132	
FT		/label= I1	
FT		/note= "cytoplasmic"	
FT	Domain	133..154	
FT		/label= TMH2	
FT		/note= "transmembrane"	
FT	Domain	155..169	
FT		/label= E2	
FT		/note= "Extracellular"	
FT	Domain	170..191	
FT		/label= TMH3	
FT		/note= "transmembrane"	
FT	Domain	192..210	
FT		/label= I2	
FT		/note= "Cytoplasmic"	
FT	Domain	211..233	
FT		/label= TMH4	
FT		/note= "transmembrane"	
FT	Domain	234..259	
FT		/label= E2	
FT		/note= "extracellular"	
FT	Domain	260..284	
FT		/label= TMH5	
FT		/note= "transmembrane"	
FT	Domain	285..312	
FT		/label= I3	
FT		/note= "Cytoplasmic"	
FT	Domain	313..336	
FT		/label= TMH6	
FT		/note= "transmembrane"	
FT	Domain	337..348	
FT		/label= E3	
FT		/note= "Extracellular"	
FT	Domain	349..370	
FT		/label= TMH7	
FT		/note= "transmembrane"	
FT	Domain	371..417	
FT		/label= C-terminus	
FT		/note= "cytoplasmic"	
FT	Disulfide_bond	168..247	
FT	Modified_site	62	/note= "potential N-glycosylation"
FT		76	/note= "potential N-glycosylation"
FT	Modified_site	382	

FT Peptide /note= "palmitate"  
FT 418..427  
FT /label= HA  
PN WO9735478-A1.  
PD 02-OCT-1997.  
PF 25-MAR-1997; U05334.  
PR 26-MAR-1996; US-622348.  
PA (REGC ) UNIV CALIFORNIA.  
PI Conklin BR;  
DR WPI; 97-502739/46.  
DR N-PSDB; T90999.  
PT Selective activation of target cell expressing modified G protein  
PT coupled receptor - allows control of cellular proliferation,  
PT especially for amplification of transfected cells in gene therapy  
PS Example 1; Page 77-79; 117pp; English.  
CC This polypeptide comprises the human G protein-coupled kappa  
CC opiod receptor (KOR) (see also W30297) flanked by N- and  
CC C-terminal sequences that facilitate the detection and  
CC purification of recombinant KOR, and especially KOR RASSLS (see  
CC W30299), i.e. a receptor activated superiorly by a synthetic  
CC ligand. A novel method for selectively activating a target cell  
CC (TC) comprises: (i) introducing into the cell a nucleic acid  
CC sequence (I) that expresses a RASSL (A) and (ii) exposing the  
CC transfected cell to small synthetic molecules (B) that bind to and  
CC activate (A), inducing the G protein coupled cellular response  
CC associated with receptor activation. (A) has: (a) decreased binding  
CC affinity for a selected natural ligand of the native receptor; (b)  
CC binding affinity for (B); and (c) is activated by binding (B)  
CC sufficiently to produce the required cellular response. Also new  
CC are: transgenic cells including heterologous (I) in the genome;  
CC cellular implants comprising a TC transfected with (I); isolated  
CC (I); and transgenic animals expressing (A). Activation of (A)  
CC results, in vitro or in vivo, in cellular proliferation, or  
CC secretion of a cellular product, particularly a heterologous  
CC therapeutic protein encoded by a second inserted nucleic acid  
CC sequence. Particularly it is used to expand the relatively few  
CC cells that are successfully transfected during gene therapy  
CC procedures. Other responses that can be regulated are cell  
CC migration and contraction, or pigment production. In transgenic  
CC animals, expression or stimulation of (A) is designed to develop  
CC cardiac arrhythmia, symptoms of bone disease, seizures, vascular  
CC contractions, dementia, neurodegeneration etc., for use as models  
CC of these diseases (claimed). The transgenic animals are also used  
CC for production of improved food products (e.g. increased calcium  
CC content in eggshells or altered fat/lean ratios) or to control  
CC fertility or induce labour.  
SQ Sequence 427 AA;

Query Match 98.3%; Score 2192; DB 27; Length 427;  
Best Local Similarity 97.6%; Pred. No. 2.86e-190;  
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 124 ytkmktatniyifnlaladalvtttmpfgstvyilmnswpfgdvclckivisidyynmftsi 183  
QY 1 YTKMKTATNIYIFNLALADALVT TTPFPQSTVYILMNSWPFGDVCLCKIVISIDYNNMFTSI 60  
Db 184 ftltmmsvdryiavchp vkaldfrt plkakini ciwllsssvgisai vlggtkvredvd 243  
QY 61 FTLTMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLSSSVGISAIVLGGIKVREDVD 120  
Db 244 viecslqfdddysswdl fmkicvfafvipvlliiivcvtlmlrlksvrl lsgsrekd 303  
QY 121 VIECCLQFPDDDYSSWDLFMKICVFIFAFVIPVLIIVCYITLMLRLKXXVRL LSGSREKD 180  
Db 304 rnlrritrlvllvvavfvvcwtpihifilvealgstshstaalssyyfci algytnssln 363  
QY 181 XNLRRIIRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFICIALGYTNSSLN 240  
Db 364 pilyafldenfkrcfrdcfplk mnerqstsrvrntvqdpayl rldidgm-nkpv 417  
QY 241 PILYAFLDENFKRCFRDFCFPLKMXMERXSTSRVRNTVQDPAYLREIDGMNKPV 295

RESULT 5  
ID W44939 standard; Protein; 380 AA.  
AC W44939;  
DT 28-OCT-1998 (first entry)  
DE Mouse kappa opiate receptor.  
KW Mouse; kappa opiate receptor; transgenic animal; mammal; identification;  
KW exon; nervous tissue; pain; drug addiction; transplant rejection;  
KW immunosuppressant; analgesic; morphine; side effect.  
OS Mus sp.  
PN WO9802534-A2.  
PD 22-JAN-1998.  
PF 11-JUL-1997; F01282.  
PR 15-JUL-1996; FR-008810.  
PA (CNRS ) CENT NAT RECH SCI.  
PI Dierich A, Kieffer BL, LeMeur M, Matthes HWD, Simonin FH;  
DR WPI; 98-110582/10.  
DR N-PSDB; V49254.  
PT Transgenic animals defective in one type of opiod receptor - used  
PT to identify agents for treatment of pain, drug addiction and  
PT transplant rejection, lacking side effects of known opiate(s)  
PS Disclosure; Fig 13; 58pp; French.  
CC This sequence represents the mouse kappa opiate receptor. The gene  
CC sequence is used to generate a transgenic non-human mammal for  
CC identifying agents for treating disorders associated with opiate  
CC receptors. In the mammal, the expression of the gene encoding the  
CC opiate receptor is modified, particularly by the deletion of an exon  
CC and/or insertion of a marker gene, e.g. the neomycin resistance gene,  
CC into the sequence. Especially the expression of the gene is altered  
CC in nervous tissue. The agents are potentially useful for treating  
CC severe pain (chronic or acute), drug addiction and/or prevention or  
CC treatment of transplant rejection (as immunosuppressants). The method  
CC may isolate and identify powerful analgesics that lack morphine-like  
CC side effects.  
SQ Sequence 380 AA;

Query Match 95.8%; Score 2136; DB 34; Length 380;  
Best Local Similarity 92.9%; Pred. No. 5.22e-185;  
Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvtttmpfgsavylmnswpfgdvclckivisidyynmftsi 145  
QY 1 YTKMKTATNIYIFNLALADALVT TTPFPQSTVYILMNSWPFGDVCLCKIVISIDYNNMFTSI 60  
Db 147 ftltmmsvdryiavchp vkaldfrt plkakini ciwllsssvgisai vlggtkvredvd 206  
QY 61 FTLTMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLSSSVGISAIVLGGIKVREDVD 120  
Db 207 viecslqfdddeyswdl fmkicvfafvipvlliiivcvtlmlrlksvrl lsgsrekd 266  
QY 121 VIECCLQFPDDDYSSWDLFMKICVFIFAFVIPVLIIVCYITLMLRLKXXVRL LSGSREKD 180  
Db 267 rnlrritrlvllvvavfvvcwtpihifilvealgstshstaalssyyfci algytnssln 326  
QY 181 XNLRRIIRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFICIALGYTNSSLN 240  
Db 327 pilyafldenfkrcfrdcfplk mnerqstsrvrntvqdpas mrdvggm-nkpv 380  
QY 241 PILYAFLDENFKRCFRDFCFPLKMXMERXSTSRVRNTVQDPAYLREIDGMNKPV 295

RESULT 6  
ID R67669 standard; Protein; 380 AA.  
AC R67669;  
DT 17-AUG-1995 (first entry)  
DE Mouse kappa opiod receptor mORK1.  
KW Mouse; kappa; delta; mu; opiod receptor; brain; primer; PCR; amplify;  
KW transmembrane domain; somatostatin; receptor; human; expression vector;  
KW truncate; chimaeric; assay; probe.  
OS Mus musculus.  
PN WO9428132-A.  
PD 08-DEC-1994.  
PF 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.



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QY      61  FTLTMSVDRIYAVCHPVKALDERTPLKAKINICIWLLSSSSVGISAIVLGGTKVREDVD 120
Db      207  viecslqfddgyswdlfmkicvfvfafvipvliiivcytlmilrlksvrlsgsrek 266
QY      121  VIECCLOFPDDYSWDLEFMKICVFIFAFVLPVLLIIVCYTLMILRLKXVRLJSGSREKD 180
Db      267  rnlrritklvlvvavfiicwtpihiilvealgstshstavlssyyficialgynssln 326
QY      181  XNLRRITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFICIALGYTNSSLN 240
Db      327  pvlvafldenkrcfrdfcfpikrmmerqstgrvrvntvqdpasmrdvvgm-nkpv 380
QY      241  PILYAFLDENFKRCFRDFCFPLKMXMERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT      9
ID      W30299 standard; Protein; 424 AA.
AC      W30299;
DT      14-APR-1998 (first entry)
DE      Human kappa opioid receptor RASSL ORL.
KW      Selective target cell activation; G protein-coupled receptor;
KW      RASSL; gene therapy; cell proliferation; kappa opioid receptor;
KW      human; transgenic animal; arrhythmia; bone disease; seizure;
KW      vascular contraction; disease model.
OS      Chimeric - Homo sapiens.
OS      Chimeric - Synthetic.
FH      Key Location/Qualifiers
FT      Peptide 1..30
FT      /label= Sig_peptide
FT      /note= "prolactin signal sequence"
FT      Peptide 31..38
FT      /label= FLAG
FT      Protein 39..414
FT      /label= KOR
FT      /note= "human kappa opioid receptor"
FT      Domain 39..95
FT      /label= N-terminus
FT      /note= "extracellular"
FT      Domain 96..122
FT      /label= TMH1
FT      /note= "transmembrane"
FT      Domain 123..132
FT      /label= I1
FT      /note= "cytoplasmic"
FT      Domain 133..154
FT      /label= TMH2
FT      /note= "transmembrane"
FT      Domain 155..169
FT      /label= E2
FT      /note= "Extracellular"
FT      Domain 170..191
FT      /label= TMH3
FT      /note= "transmembrane"
FT      Domain 192..210
FT      /label= I2
FT      /note= "Cytoplasmic"
FT      Domain 211..233
FT      /label= TMH4
FT      /note= "transmembrane"
FT      Domain 234..259
FT      /label= E2
FT      /note= "extracellular, contains 17 amino acid
FT      residues from delta opiod receptor
FT      (Val-235, Gln-237, Pro-238, Asp-240,
FT      Gly-241, Ala-242, Val-243, Val-244,
FT      Thr-246, Ser-251, Pro-252, Ser-253,
FT      Trp-254, Tyr-255, Thr-258, Val-259,
FT      Thr-260);"
FT      Domain 260..281
FT      /label= TMH5
FT      /note= "transmembrane"
FT      Domain 282..309
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FT      /label= I3
FT      /note= "Cytoplasmic"
FT      Domain 310..333
FT      /label= TMH6
FT      /note= "Transmembrane"
FT      Domain 334..345
FT      /label= E3
FT      /note= "Extracellular"
FT      Domain 346..367
FT      /label= TMH7
FT      /note= "transmembrane"
FT      Domain 368..414
FT      /label= C-terminus
FT      /note= "cytoplasmic"
FT      Disulfide_bond 168..245
FT      Modified_site 62
FT      /note= "potential N-glycosylation"
FT      Modified_site 76
FT      /note= "potential N-glycosylation"
FT      Modified_site 382
FT      /note= "palmitate"
FT      Peptide 415..424
FT      /label= HA
FT      W09735478-A1.
FT      02-OCT-1997.
PD      25-MAR-1997; U05334.
PF      26-MAR-1996; US-622348.
PR      (REGC ) UNIV CALIFORNIA.
PA      Conklin BR;
DR      WPI; 97-502739/46.
DR      N-PSDB; T92601.
PT      Selective activation of target cell expressing modified G protein
PT      coupled receptor - allows control of cellular proliferation,
PT      especially for amplification of transfected cells in gene therapy
PS      Example 1; Page 80-82; 117pp; English.
CC      This protein comprises RASSL ORL, a G protein-coupled receptor that
CC      is activated superiorly by synthetic ligands. ORL comprises human
CC      G protein-coupled kappa opioid receptor (KOR) (see also W30297)
CC      modified at 17 amino acid positions to contain the corresponding
CC      amino acid of the delta opioid receptor, and containing N- and
CC      C-terminal flanking sequences that facilitate the detection and
CC      purification of recombinant protein. A novel method for selectively
CC      activating a target cell (TC) comprises: (i) introducing into the
CC      cell a nucleic acid sequence (I) (see T92601) that expresses a RASSL
CC      (A) and (ii) exposing the transfected cell to small synthetic molecules
CC      (B) that bind to and activate (A), inducing the G protein coupled
CC      cellular response associated with receptor activation. (A) has: (a)
CC      decreased binding affinity for a selected natural ligand of the
CC      native receptor; (b) binding affinity for (B); and (c) is activated
CC      by binding (B) sufficiently to produce the required cellular response.
CC      Also new are: transgenic cells including heterologous (I) in the
CC      genome; cellular implants comprising a TC transfected with (I);
CC      isolated (I); and transgenic animals expressing (A). Activation of
CC      (A) results, in vitro or in vivo, in cellular proliferation, or
CC      secretion of a cellular product, particularly a heterologous
CC      therapeutic protein encoded by a second inserted nucleic acid
CC      sequence. Particularly it is used to expand the relatively few
CC      cells that are successfully transfected during gene therapy
CC      procedures. Other responses that can be regulated are cell
CC      migration and contraction, or pigment production. In transgenic
CC      animals, expression or stimulation of (A) is designed to develop
CC      cardiac arrhythmia, symptoms of bone disease, seizures, vascular
CC      contractions, dementia, neurodegeneration etc., for use as models
CC      of these diseases (claimed). The transgenic animals are also used
CC      for production of improved food products (e.g. increased calcium
CC      content in eggshells or altered fat/lean ratios) or to control
CC      fertility or induce labour.
SQ      Sequence 424 AA;
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Query Match 90.1%; Score 2008; DB 27; Length 424;  
Best Local Similarity 91.2%; Pred.No. 5.44e-173;  
Matches 269; Conservative 4; Mismatches 18; Indels 4; Gaps 4;









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Release 3.1A John F. Collins, Biocomputing Research Unit.  
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Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run On: Thu Feb 17 11:17:17 2000; MasPar time 7.39 Seconds  
Tabular output not generated. 517.015 Million cell updates/sec

Title: >US-08-455-683-12  
Description: (1-295) from US08455683.pap  
Perfect Score: 2229  
Sequence: 1 YTKMKTATNIYIFNLALADA.....NTVQDPAYLREIDGMNKPV 295

Scoring table: PAM 150  
Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 31.719; Variance 152.161; scale 0.208

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				%	
Result No.	Score	Query Match	Length DB ID	Description	Pred. No.
1	2123	95.2	380 1	US-08-149- Sequence 7, Applicatio	1.68e-175
2	2123	95.2	380 2	US-08-911- Sequence 7, Applicatio	1.68e-175
3	1990	89.3	378 2	US-08-514- Sequence 10, Applicati	1.28e-163
4	1522	68.3	391 2	US-08-454- Sequence 3, Applicatio	6.69e-122
5	1522	68.3	400 3	PCT-US94-1 Sequence 8, Applicatio	6.69e-122
6	1520	68.2	398 1	US-08-149- Sequence 5, Applicatio	1.01e-121
7	1520	68.2	398 2	US-08-911- Sequence 5, Applicatio	1.01e-121
8	1520	68.2	398 3	PCT-US94-1 Sequence 2, Applicatio	1.01e-121
9	1452	65.1	367 2	US-08-454- Sequence 4, Applicatio	1.12e-115
10	1451	65.1	372 2	US-08-911- Sequence 6, Applicatio	1.37e-115
11	1451	65.1	372 1	US-08-149- Sequence 6, Applicatio	1.37e-115
12	1448	65.0	372 2	US-08-411- Sequence 2, Applicatio	2.53e-115
13	1448	65.0	372 2	US-08-411- Sequence 10, Applicati	2.53e-115
14	1426	64.0	398 2	US-08-514- Sequence 8, Applicatio	2.28e-113
15	1385	62.1	330 2	US-08-454- Sequence 5, Applicatio	9.99e-110
16	1345	60.3	367 2	US-08-454- Sequence 2, Applicatio	3.54e-106
17	1345	60.3	367 3	PCT-US94-1 Sequence 17, Applicati	3.54e-106
18	1344	60.3	372 2	US-08-514- Sequence 9, Applicatio	4.35e-106
19	1335	59.9	367 1	US-08-149- Sequence 4, Applicatio	2.73e-105
20	1335	59.9	367 2	US-08-553- Sequence 4, Applicatio	2.73e-105
21	1335	59.9	367 2	US-08-514- Sequence 4, Applicatio	2.73e-105
22	1335	59.9	367 2	US-08-911- Sequence 4, Applicatio	2.73e-105
23	1230	55.2	367 2	US-08-514- Sequence 7, Applicatio	5.54e-96

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25	830	37.2	391	1	US-08-417-	Sequence 4, Applicatio	1.01e-60
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29	830	37.2	391	1	US-07-816-	Sequence 4, Applicatio	1.01e-60
30	788	35.4	369	2	US-08-411-	Sequence 3, Applicatio	4.78e-57
31	785	35.2	369	1	US-07-816-	Sequence 8, Applicatio	8.74e-57
32	785	35.2	369	1	US-08-417-	Sequence 8, Applicatio	8.74e-57
33	780	35.0	369	1	US-08-417-	Sequence 16, Applicati	2.39e-56
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40	683	30.6	418	1	US-07-816-	Sequence 10, Applicati	6.90e-48
41	661	29.7	328	1	US-08-148-	Sequence 2, Applicatio	5.64e-46
42	623	27.9	211	2	US-08-771-	Sequence 19, Applicati	1.12e-42
43	623	27.9	211	1	US-07-915-	Sequence 19, Applicati	1.12e-42
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RESULT 1

US-08-149-093A-7

STANDARD;

PRT;

380 AA.

ALIGNMENTS

Sequence 7, Application US/08149093A

Sequence 7, Application US/08149093A

Patent No. 5658783

GENERAL INFORMATION:

APPLICANT: Bunzow, James R

APPLICANT: Grandy, David K

TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific

TITLE OF INVENTION: Opioid Receptor Gene and Uses

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,093A

FILING DATE: 06-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5658783nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,311

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 380 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

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CC CC FEATURE:
CC CC NAME/KEY: Protein
CC CC LOCATION: 1..380
CC CC OTHER INFORMATION: /label= Identifier
CC CC OTHER INFORMATION: /note= "Mouse Kappa-Opioid Receptor"
CC CC SEQUENCE 380 AA; 42652 MW; 802929 CN;

Query Match 95.2%; Score 2123; DB 1; Length 380;
Best Local Similarity 92.2%; Pred. No. 1.68e-175;
Matches 272; Conservative 13; Mismatches 9; Indels 1; Gaps 1;

Db 87 YTKMKTATNIYIFNLALADALVTTTTPFQSAVYLMNSWPFQDVLCKIVISIDYNNMFTSI 146
QY 1 YTKMKTATNIYIFNLALADALVTTTTPFQSTVYLMNSWPFQDVLCKIVISIDYNNMFTSI 60

Db 147 FTLTMSVDRIYAVCHPVKALDFRTPKAKIINICIWLLASSVGISAIVLGGTKVREDVD 206
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPKAKIINICIWLLSSSVGISAIVLGGTKVREDVD 120

Db 207 VIECSLOFPDDDEYSWDLFMKICVFFAFVFPVLIIVCYTLMILRLKSVRLLSGSREKD 266
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Db 267 RNLRRITKLIVLVVAVFIIICWTPIHIFILVEALGSTSHSTAALSSYFFCAILGYTNSSLN 326
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RESULT 2
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DE Sequence 7, Application US/08911245
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CC Sequence 7, Application US/08911245
CC Patent No. 5821067
CC GENERAL INFORMATION:
CC APPLICANT: Bunzow, James R
CC APPLICANT: Grandy, David K
CC TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
CC TITLE OF INVENTION: Opioid Receptor Gene and Uses
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Banner & Allegretti, Ltd.
CC STREET: 10 South Wacker Drive, Suite 3000
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/911,245
CC FILING DATE: 15-AUG-1997
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/149093
CC FILING DATE: 06-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5821067nan, Kevin E
CC REGISTRATION NUMBER: 35,303
CC REFERENCE/DOCKET NUMBER: 93,311
CC TELECOMMUNICATION INFORMATION:
```

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CC CC TELEPHONE: 312-715-1000
CC CC TELEFAX: 312-715-1234
CC CC TELEX: 910-221-5317
CC CC INFORMATION FOR SEQ ID NO: 7:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 380 amino acids
CC CC TYPE: amino acid
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
CC CC FEATURE:
CC CC NAME/KEY: Protein
CC CC LOCATION: 1..380
CC CC OTHER INFORMATION: /label= Identifier
CC CC OTHER INFORMATION: /note= "Mouse Kappa-Opioid Receptor"
CC CC SEQUENCE 380 AA; 42652 MW; 802929 CN;

Query Match 95.2%; Score 2123; DB 2; Length 380;
Best Local Similarity 92.2%; Pred. No. 1.68e-175;
Matches 272; Conservative 13; Mismatches 9; Indels 1; Gaps 1;

Db 87 YTKMKTATNIYIFNLALADALVTTTTPFQSAVYLMNSWPFQDVLCKIVISIDYNNMFTSI 145
QY 1 YTKMKTATNIYIFNLALADALVTTTTPFQSTVYLMNSWPFQDVLCKIVISIDYNNMFTSI 60

Db 147 FTLTMSVDRIYAVCHPVKALDFRPLKAKIINICIWLLASSVGISAIVLGGTKVREDVD 205
QY 61 FTLTMSVDRIYAVCHPVKALDFRPLKAKIINICIWLLSSSVGISAIVLGGIKVREDVD 120

Db 207 VIECSLOFPDDDEYSWDLFMKICVFFAFVFPVLIIVCYTLMILRLKSVRLLSGSREKD 265
QY 121 VIECCLQFPDDDYSWDLFMKICVFFAFVFPVLIIVCYTLMILRLKXVRLLSGSREKD 180

Db 267 RNLRRITKLIVLVVAVFIIICWTPIHIFILVEALGSTSHSTAALSSYFFCAILGYTNSSLN 326
QY 181 XNLRRIITRLVLVWVAVFVVCWTPHIFILVEALGSTSHSTAALSSYFFCIAIGYTNSSLN 240

Db 327 PVLVYAFLDENFKRCFRDFCFPIKMMERQSTNRVRNTVQDPASMRDVGGM-NKPV 380
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RESULT 3
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DE Sequence 10, Application US/08514451A
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CC Sequence 10, Application US/08514451A
CC Patent No. 5837809
CC GENERAL INFORMATION:
CC APPLICANT: Bunzow, James R.
CC APPLICANT: Grandy, David K.
CC APPLICANT: Civeilli, Olivier
CC APPLICANT: Reinscheid, Rainer K.
CC APPLICANT: No. 5837809hacker, Hans-Peter
CC APPLICANT: Monsma, Frederick J.
CC TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID
CC TITLE OF INVENTION: RECEPTOR LIGAND AND USES
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Klarquist Sparkman Campbell
CC ADDRESSEE: Leigh & Whinston LLP
CC STREET: 121 S.W. Salmon, Suite 1600
CC CITY: Portland
CC STATE: Oregon
CC COUNTRY: USA
CC ZIP: 97204
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy Disk
CC COMPUTER: IBM PC compatible
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CC GENERAL INFORMATION:
CC APPLICANT: Bunzow, James R
CC APPLICANT: Grandy, David K
CC TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
CC TITLE OF INVENTION: Opioid Receptor Gene and Uses
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Banner & Allegretti, Ltd.
CC STREET: 10 South Wacker Drive, Suite 3000
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/911,245
CC FILING DATE: 15-AUG-1997
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/149093
CC FILING DATE: 06-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5821067nan, Kevin E
CC REGISTRATION NUMBER: 35,303
CC REFERENCE/DOCKET NUMBER: 93,311
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-715-1000
CC TELEFAX: 312-715-1234
CC TELEX: 910-221-5317
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 398 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..398
CC OTHER INFORMATION: /label= Identifier
CC OTHER INFORMATION: /note= "Rat Mu-Opioid Receptor"
SQ SEQUENCE 398 AA; 44508 MW; 870781 CN;

Query Match 68.2%; Score 1520; DB 2; Length 398;
Best Local Similarity 65.7%; Pred. No. 1.01e-121;
Matches 190; Conservative 46; Mismatches 49; Indels 4; Gaps 4;

Db 96 YTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFPGTILCKIVISIDYNNMFTSI 155
QY 1 YTKMKTATNIYIFNLALADALVTTTTPFQSVYLMNSWPFQDVLCIKIVISIDYNNMFTSI 60

Db 156 FTLCTMSVDRIYIAVCHPVKALDFRTPRNAKIVNVCNWLSSAIGLPVMEFATKYRQG-S 214
QY 61 FTLTMSVDRIYIAVCHPVKALDFRTPLKAKIINICITWLLSSVGSIAIVLGGTKVREDVD 120

Db 215 -IDCTLTFSHPTW-YWENLLKICVFIFAFIMPILITVCYGLMILRLKSVRLSGSKEKD 272
QY 121 VIECCLOFPDDDDYSWWDLEFMKICVFIFAFVPLVLIIVCYTLMILRLKXVRLSGSREKD 180

Db 273 RNLRRITRMVLVVAVFVVCWTPPIHIYVILKALITPETTFQTVSWHFCIALGYTNSCLN 332
QY 181 XNLRITRLVLVVAVFVVCWTPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN 240

Db 333 PVLAFLDENFKRCFRCFICPTSSSTIEQQNSTVRQNTREHPSTANTVD 381
QY 241 PILYAFLDENFKRCFRDCEPLKMXMERXSTSRVR-NTVQDPAYLREID 288

RESULT 8
ID PCT-US94-10358-2 STANDARD; PRI; 398 AA.
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CC Sequence 2, Application PC/TUS9410358
CC Sequence 2, Application PC/TUS9410358
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P. O. Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
CC SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/10358
CC FILING DATE: Concurrently herewith
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/120.601
CC FILING DATE: 13 SEPTEMBER 1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILSON, MARK B.
CC REGISTRATION NUMBER: 37,259
CC REFERENCE/DOCKET NUMBER: INDA005P--
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (512) 418-3000
CC TELEFAX: (713) 789-2679
CC TELEX: 79-0924
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 398 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 398 AA; 44508 MW; 870781 CN;

Query Match 68.2%; Score 1520; DB 3; Length 398;
Best Local Similarity 65.7%; Pred. No. 1.01e-121;
Matches 190; Conservative 46; Mismatches 49; Indels 4; Gaps 4;

Db 96 YTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFPGTILCKIVISIDYNNMFTSI 155
QY 1 YTKMKTATNIYIFNLALADALVTTTTPFQSVYLMNSWPFQDVLCIKIVISIDYNNMFTSI 60

Db 156 FTLCTMSVDRIYIAVCHPVKALDFRTPRNAKIVNVCNWLSSAIGLPVMEFATKYRQG-S 214
QY 61 FTLTMSVDRIYIAVCHPVKALDFRTPLKAKIINICITWLLSSVGSIAIVLGGTKVREDVD 120

Db 215 -IDCTLTFSHPTW-YWENLLKICVFIFAFIMPILITVCYGLMILRLKSVRLSGSKEKD 272
QY 121 VIECCLOFPDDDDYSWWDLEFMKICVFIFAFVPLVLIIVCYTLMILRLKXVRLSGSREKD 180

Db 273 RNLRRITRMVLVVAVFVVCWTPPIHIYVILKALITPETTFQTVSWHFCIALGYTNSCLN 332
QY 181 XNLRITRLVLVVAVFVVCWTPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN 240

Db 333 PVLAFLDENFKRCFRCFICPTSSSTIEQQNSTVRQNTREHPSTANTVD 381
QY 241 PILYAFLDENFKRCFRDCEPLKMXMERXSTSRVR-NTVQDPAYLREID 288

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ID US-08-454-549-4 STANDARD; PRT; 367 AA.  
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Sequence 4, Application US/08454549  
Sequence 4, Application US/08454549  
Patent No. 5866324  
GENERAL INFORMATION:  
APPLICANT: EPPLER, C. Mark  
APPLICANT: OZENBERGER, Bradley A.  
APPLICANT: HULMES, Jeffrey D.  
TITLE OF INVENTION: cDNA's ENCODING PROTEINS CLOSELY RELATED  
TITLE OF INVENTION: TO OPIOID RECEPTORS  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby, P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/454,549  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robinson, Joseph R.  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 0646/1A818-US5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 527-7700  
TELEFAX: (212) 753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 367 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Rat  
SEQUENCE 367 AA; 40122 MW; 712609 CN;  
Query Match 65.1%; Score 1452; DB 2; Length 367;  
Best Local Similarity 68.8%; Pred. No. 1.12e-115;  
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;  
Db 77 YTKLKTATNIYIFNLALADALATSTLPFQSAKYLMTWPFGEELCKAVLSIDYNNMFTSI 136  
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Db 137 FTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGPIMVMVAVTQPRDGA- 195  
FTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGPIMVMVAVTQPRDGA- 195  
QY 61 FTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGPIMVMVAVTQPRDGA- 120  
FTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGPIMVMVAVTQPRDGA- 120  
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QY 121 VIECCLOQFPDDYSWWDLFMKICVFIFAFVIPVLIIVCYITLMLRLKXVRLLSGSREKD 180  
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QY 181 XNLRRITRLVLVVVAVFVVCWTPIHIFILVEALGSTSHSTA-ALSSYFFCIALGYTNSSL 239  
Db 314 NPVLYAFLDENFKRCFRQLC 333

QY 240 NPILYAFLDENFKRCFRDFC 259  
RESULT 10  
ID US-08-911-245-6 STANDARD; PRT; 372 AA.  
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Sequence 6, Application US/08911245  
Sequence 6, Application US/08911245  
Patent No. 5821067  
GENERAL INFORMATION:  
APPLICANT: Bunzow, James R  
APPLICANT: Grandy, David K  
TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific  
TITLE OF INVENTION: Opioid Receptor Gene and Uses  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,245  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/149093  
FILING DATE: 06-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5821067nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 93,311  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 372 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..372  
OTHER INFORMATION: /label= Identifier  
OTHER INFORMATION: /note= "Mouse Delta-Opioid Receptor"  
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Best Local Similarity 69.6%; Pred. No. 1.37e-115;  
Matches 181; Conservative 42; Mismatches 33; Indels 4; Gaps 4;  
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QY 1 YTKMKTATNIYIFNLALADALVTTTTPFQSTVYLMNSWPFQDVLCVKIVISIDYNNMFTSI 60  
Db 137 FTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGPIMVMVAVTQPR-DFA 195  
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QY 61 FTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGPIMVMVAVTQPRDGA- 120  
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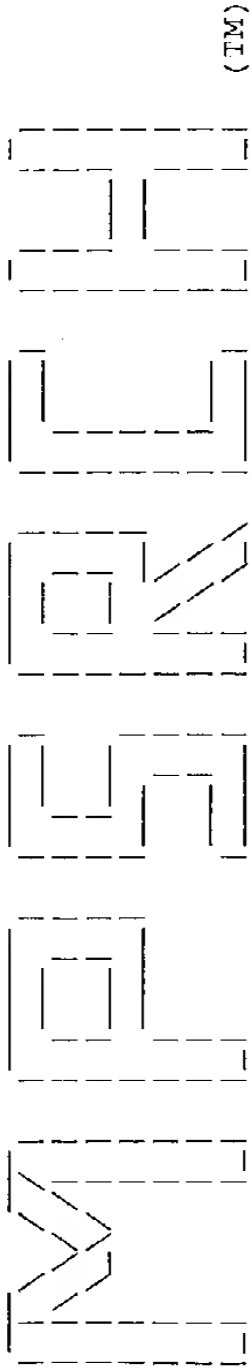


CC NAME: William D. No. 5837809nan, M.D.  
CC REGISTRATION NUMBER: 30,878  
CC REFERENCE/DOCKET NUMBER: 899-45995/WDN  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (503) 226-7391  
CC TELEFAX: (503) 228-9446  
CC INFORMATION FOR SEQ ID NO: 8:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 398 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE:  
CC DESCRIPTION: peptide  
CC SEQUENCE 398 AA; 44467 MW; 888796 CN;  
  
Query Match 64.0%; Score 1426; DB 2; Length 398;  
Best Local Similarity 62.6%; Pred. No. 2.28e-113;  
Matches 181; Conservative 46; Mismatches 58; Indels 4; Gaps 4;  
  
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QY 61 FTLCMTMSVDRIYAVCHPVKALDPRTPKAKIINICIWLLSSVGSIAVLGGTKVREDVD 120  
  
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QY 121 VIECCLOFPDDDDYSWWDLEFMKICVFIFAFAVPLIIIVCYTLMILRLKXXVRLLSGSREKD 180  
  
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Db 333 PVLVAFLDKMTKRCRTREFCIPSTSTIEQQNSIRVRQNTREHPSTANTVD 381  
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CC Sequence 5, Application US/08454549  
CC Sequence 5, Application US/08454549  
CC Patent No. 5866324  
CC GENERAL INFORMATION:  
CC APPLICANT: EPPLER, C. Mark  
CC APPLICANT: OZENBERGER, Bradley A.  
CC APPLICANT: HULMES, Jeffrey D.  
CC TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED  
CC TITLE OF INVENTION: TO OPIOID RECEPTORS  
CC NUMBER OF SEQUENCES: 13  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Darby & Darby, P.C.  
CC STREET: 805 Third Avenue  
CC CITY: New York  
CC STATE: New York  
CC COUNTRY: USA  
CC ZIP: 10022  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/454,549  
CC FILING DATE: 30-MAY-1995

CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robinson, Joseph R.  
CC REGISTRATION NUMBER: 33,448  
CC REFERENCE/DOCKET NUMBER: 0646/1A818-US5  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (212) 527-7700  
CC TELEFAX: (212) 753-6237  
CC TELEX: 236687  
CC INFORMATION FOR SEQ ID NO: 5:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 330 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: not relevant  
CC TOPOLOGY: not relevant  
CC MOLECULE TYPE: protein  
CC ORIGINAL SOURCE:  
CC ORGANISM: Rat  
CC SEQUENCE 330 AA; 36851 MW; 611728 CN;  
  
Query Match 62.1%; Score 1385; DB 2; Length 330;  
Best Local Similarity 87.6%; Pred. No. 9.99e-110;  
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QY 154 LIIIVCYTLMILRLKXXVRLLSGSREKDXNLRRITRLVLVVAVFVVCWTPIHIFILVEAL 213  
  
Db 250 GSTSHSTAVLSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNR 309  
QY 214 GSTSHSTAALSSYYFCIALGYTNSSLNPILYAFLDENFKRCFRDFCFPLKMXMERXSTSR 273  
  
Db 310 VRNTVQDPASMRDVGGM-NKPV 330  
QY 274 VRNTVQDPAYLREIDGMMNKPV 295  
  
Search completed: Thu Feb 17 11:17:26 2000  
Job time : 9 secs.



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Release 3.1A John F. Collins, Biocomputing Research Unit,  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 17 11:15:32 2000; MasPar time 15.81 Seconds  
Tabular output not generated. 747.854 Million cell updates/sec

Title: >US-08-455-683-12  
Description: (1-295) from US08455683.pep  
Perfect Score: 2229  
Sequence: 1 YTKMKTATNIYIFNLALADA.....NTVQDPAYLREIDGMNKPV 295

Scoring table: PAM 150  
Gap 11  
Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir60  
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 47.368; Variance 110.368; scale 0.429

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2192	98.3	380	2 JC2338	kappa opioid receptor	0.00e+00
2	2192	98.3	380	2 I57005	opioid receptor kappa	0.00e+00
3	2157	96.8	380	2 A55259	kappa opioid receptor	0.00e+00
4	2136	95.8	380	2 A48227	kappa opioid receptor	0.00e+00
5	2132	95.6	380	2 S36143	kappa opioid receptor	0.00e+00
6	2114	94.8	380	2 JC2434	kappa-opioid receptor	0.00e+00
7	1524	68.4	398	2 A57510	mu opioid receptor	8.97e-243
8	1523	68.3	373	2 JE0087	delta opioid receptor	1.36e-242
9	1522	68.3	400	2 I56553	opiate receptor mu	2.06e-242
10	1520	68.2	392	2 S65693	opioid receptor mu va	4.75e-242
11	1520	68.2	398	2 I56517	mu-opioid receptor	4.75e-242
12	1505	67.5	398	2 I56504	mu opioid receptor	2.45e-239
13	1458	65.4	372	2 I38657	delta opiate receptor	7.65e-231
14	1458	65.4	372	2 I38532	delta opioid receptor	7.65e-231
15	1452	65.1	372	2 S34592	delta opioid receptor	9.28e-230
16	1448	65.0	372	2 B48227	delta opioid receptor	4.90e-229
17	1345	60.3	367	2 I56520	G protein-coupled rec	1.86e-210
18	1343	60.3	367	2 JC2421	opioid receptor homol	4.27e-210
19	1342	60.2	367	2 I49022	opioid receptor	6.47e-210
20	1331	59.7	370	2 S43087	K3 opiate receptor	6.19e-208
21	830	37.2	391	2 A39297	orphan opioid recepto	1.66e-118
22	830	37.2	391	2 C41795	somatostatin receptor	1.66e-118
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24	822	36.9	384	2 A47249	brain-specific somato	4.26e-117
25	816	36.6	388	2 JN0605	somatostatin receptor	4.86e-116
26	810	36.3	384	2 JC4629	somatostatin receptor	5.54e-115
27	789	35.4	369	2 JC2083	somatostatin receptor	2.74e-111
28	788	35.4	369	2 A45291	somatostatin receptor	4.11e-111
29	785	35.2	369	2 D41795	somatostatin receptor	1.38e-110
30	781	35.0	346	2 S29248	somatostatin receptor	6.98e-110
31	780	35.0	369	2 B41795	somatostatin receptor	1.05e-109
32	736	33.0	333	2 I38974	G protein-coupled rec	5.43e-102
33	683	30.6	418	2 A46226	somatostatin receptor	9.74e-93
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38	601	27.0	428	2 S30508	probable G protein-co	1.60e-78
39	599	26.9	428	2 A44021	somatostatin receptor	3.53e-78
40	545	24.5	349	2 I59336	galanin receptor 1	6.66e-69
41	531	23.8	72	2 G01546	opioid receptor kappa	1.64e-66
42	513	23.0	387	3 JC5949	galanin receptor 2	1.92e-63
43	496	22.3	355	2 A45177	chemokine (C-C) recep	1.48e-60
44	496	22.3	359	2 S44425	angiotensin II recept	1.48e-60
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ALIGNMENTS

RESULT 1  
ENTRY JC2338 #type complete  
TITLE kappa opioid receptor - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 10-Sep-1997  
ACCESSIONS JC2338; A55354  
REFERENCE JC2338  
#authors Mansson, E.; Bare, L.; Yang, D.  
#journal Biochem. Biophys. Res. Commun. (1994) 202:1431-1437  
#title Isolation of a human kappa opioid receptor cDNA from placenta.  
#cross-references MUID:94338360  
#accession JC2338  
#molecule\_type mRNA  
#residues 1-380 #label MAN  
#experimental\_source placenta  
REFERENCE A55354  
#authors Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhl, G.R.  
#journal J. Biol. Chem. (1994) 269:25966-25969  
#title Human kappa opiate receptor second extracellular loop elevates dynorphin's affinity for human mu/kappa chimeras.  
#cross-references MUID:95014415  
#accession A55354  
#status preliminary  
#molecule\_type mRNA  
#residues 136-279 #label WAN  
#cross-references GB:L36130; NID:g598184; PID:g598185  
COMMENT This receptor preferentially binds to dynorphins.  
KEYWORDS G protein-coupled receptor; receptor; transmembrane protein  
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95-114 #domain transmembrane #status predicted #label TM2\  
133-154 #domain transmembrane #status predicted #label TM3\  
177-199 #domain transmembrane #status predicted #label TM4\  
228-251 #domain transmembrane #status predicted #label TM5\  
275-296 #domain transmembrane #status predicted #label TM6\  
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Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 87 YTKMKTATNIYIFNLALADALVTITMPFQSTVILMNSWPGDVLCKIVISIDYNNMFTSI 146  
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GENETICS  
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KEYWORDS brain; G protein-coupled receptor; glycoprotein; opioid peptide; phosphoprotein; transmembrane protein  
SUMMARY #length 380 #molecular-weight 42652 #checksum 9937

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Best Local Similarity 92.9%; Pred. No. 0.00e+00;  
Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

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QY 121 VIECCLQFPDDDDYSWDLFMKICVVFVAFVPIVLIIVCYTLMILRLKXXVRLLSGSREXD 180

Db 267 RNLRRITKLVVAVVAVFIICWTPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN 326  
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QY 181 XNLRRIITRLVAVVAVFVVCWTPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN 240

Db 327 PVLVAFLDENFKRCRDFCFPIKMMERQSTNRVNTVQDPASMRDVGGM-NKPV 380  
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QY 241 PILVAFLDENFKRCRDFCFPLKMMERXSTSRVNTVQDPAYLREIDGMMNKPV 295

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TITLE kappa opioid receptor - rat  
ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 10-Dec-1993 #sequence\_revision 19-Oct-1995 #text\_change 29-Jan-1999

ACCESSIONS S36143; S38825; S36102; S39015; A48789  
REFERENCE S36143  
#authors Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, K.  
#journal FEBS Lett. (1993) 330:77-80  
#title cDNA cloning and pharmacological characterization of an opioid receptor with high affinities for kappa-subtype-selective ligands.  
#cross-references MUID:93380575  
#accession S36143

#status preliminary  
#molecule\_type mRNA  
#residues 1-380 #label NIS  
#cross-references GB:D16534; NID:g409390; PID:d1004487; PID:g415310

REFERENCE S38825  
#authors Chen, Y.; Mestek, A.; Liu, J.; Yu, L.  
#journal Biochem. J. (1993) 295:625-628  
#title Molecular cloning of a rat kappa opioid receptor reveals sequence similarities to the mu and delta opioid receptors.  
#accession S38825

#status preliminary  
#molecule\_type mRNA  
#residues 1-380 #label CHE  
#cross-references GB:I22001; NID:g409236; PID:g409237

REFERENCE S36102  
#authors Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.; Onogi, T.; Kaneko, S.; Satoh, M.  
#journal FEBS Lett. (1993) 329:291-295  
#title Cloning and expression of a cDNA for the rat kappa-opioid receptor.  
#cross-references MUID:93374033  
#accession S36102

#molecule\_type mRNA  
#residues 1-41, 'L', 43-380 #label MIN  
#cross-references GB:D16829; NID:g404115; PID:d1004628; PID:g404116

REFERENCE S39015  
#authors Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Dieriel, J.K.; Ashby,

B.; Liu-Chen, L.Y.  
Biochem. J. (1993) 295:629-633  
Molecular cloning and expression of a rat kappa opioid receptor.  
#accession S39015

#molecule\_type mRNA  
#residues 1-344, 'Y', 346-380 #label LIS  
REFERENCE A48789  
#authors Meng, F.; Xie, G.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9954-9958  
#title Cloning and pharmacological characterization of a rat kappa opioid receptor.  
#cross-references MUID:94052210  
#accession A48789

#status preliminary; translated from GB/EMBL/DDBJ  
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#cross-references EMBL:U00442; NID:g403486; PID:g403487  
KEYWORDS G protein-coupled receptor; transmembrane protein  
SUMMARY #length 380 #molecular-weight 42688 #checksum 9972

Query Match 95.6%; Score 2132; DB 2; Length 380;  
Best Local Similarity 92.5%; Pred. No. 0.00e+00;  
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 YTKMKTATNIYIFNLALADALVTTTTPFQSAVYLMNSWPFQDVLCCKIVISIDYNNMFTSI 146  
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QY 1 YTKMKTATNIYIFNLALADALVTTTTPFQSTVYLMNSWPFQDVLCCKIVISIDYNNMFTSI 60

Db 147 FTLTMSVDRIYIAVCHPVKALDFRPLKAKIINICIWLASSVGSISAIVLGGTKVREDVD 206  
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QY 61 FTLTMSVDRIYIAVCHPVKALDFRPLKAKIINICIWLSSSVGSISAIVLGGTKVREDVD 120

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Db 267 RNLRRITKLVVAVVAVFIICWTPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN 326  
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TITLE kappa-opioid receptor - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 05-Apr-1995

ACCESSIONS JC2434  
REFERENCE JC2434  
#authors Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi, T.

#journal Biochem. Biophys. Res. Commun. (1994) 205:1353-1357  
#title Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor and an opioid receptor homologue (MOR-C).  
#cross-references MUID:95100967  
#accession JC2434

#molecule\_type mRNA  
#residues 1-380 #label NIS  
#cross-references DDBJ:D31563

GENETICS  
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#introns 86/2; 204/1  
KEYWORDS receptor  
SUMMARY #length 380 #molecular-weight 42630 #checksum 9705

Query Match 94.8%; Score 2114; DB 2; Length 380;  
Best Local Similarity 92.5%; Pred. No. 0.00e+00;









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Query Match            65.1%;   Score 1452;   DB 2;   Length 372;  
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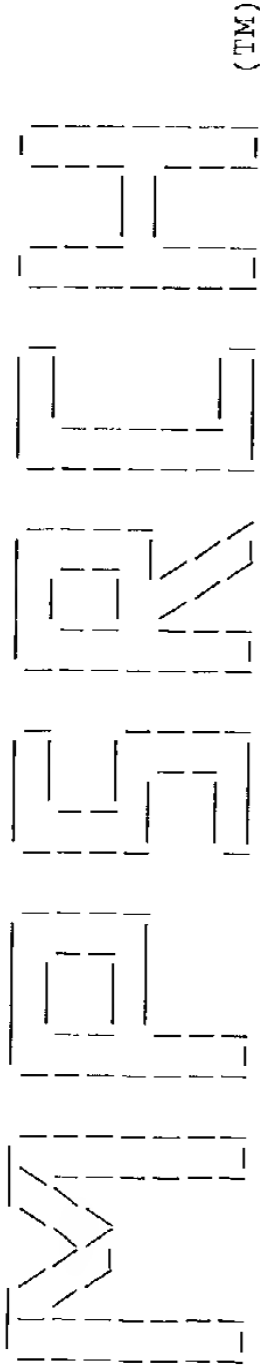
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QY     181   XNLRITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTA-ALSSYYFCIALGYTNSSL 239

Db     314   NPVLYAFLDENFKRCRQLC 333  
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY     240   NPILYAFLDENFKRCRDFC 259

Search completed: Thu Feb 17 11:15:49 2000  
Job time : 17 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Feb 17 11:16:07 2000; MasPar time 10.89 Seconds  
Tabular output not generated. 766.047 Million cell updates/sec

Title: >US-08-455-683-12  
Description: (1-295) from US08455683.pep  
Perfect Score: 2229  
Sequence: 1 YTKMKTATNIYIFNLALADA.....NTVQDPAYLREIDGMNKPV 295

Scoring table: PAM 150  
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot37  
1:swissprot

Statistics: Mean 48.475; Variance 96.994; scale 0.500

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2192	98.3	380	1	OPRK_HUMAN KAPPA-TYPE OPIOID RECE	0.00e+00
2	2157	96.8	380	1	OPRK_CAVPO KAPPA-TYPE OPIOID RECE	0.00e+00
3	2136	95.8	380	1	OPRK_MOUSE KAPPA-TYPE OPIOID RECE	0.00e+00
4	2132	95.6	380	1	OPRK_RAT KAPPA-TYPE OPIOID RECE	0.00e+00
5	1524	58.4	398	1	OPRM_MOUSE MU-TYPE OPIOID RECEPTO	2.17e-282
6	1522	58.3	398	1	OPRM_RAT MU-TYPE OPIOID RECEPTO	5.72e-282
7	1522	58.3	400	1	OPRM_HUMAN MU-TYPE OPIOID RECEPTO	5.72e-282
8	1518	68.1	401	1	OPRM_PIG MU-TYPE OPIOID RECEPTO	3.97e-281
9	1489	66.8	401	1	OPRM_BOVIN MU-TYPE OPIOID RECEPTO	5.00e-275
10	1458	65.4	372	1	OPRD_HUMAN DELTA-TYPE OPIOID RECE	1.64e-268
11	1452	65.1	372	1	OPRD_RAT DELTA-TYPE OPIOID RECE	2.99e-267
12	1448	65.0	372	1	OPRD_MOUSE DELTA-TYPE OPIOID RECE	2.07e-266
13	1345	60.3	367	1	OPRX_RAT NCCICEPTIN RECEPTOR (O	8.49e-245
14	1343	60.3	367	1	OPRX_MOUSE NOCICEPTIN RECEPTOR (O	2.23e-244
15	1331	59.7	370	1	OPRX_HUMAN NOCICEPTIN RECEPTOR (O	7.28e-242
16	1327	59.5	370	1	OPRX_PIG NOCICEPTIN RECEPTOR (O	5.01e-241
17	1319	59.2	370	1	OPRX_CAVPO NOCICEPTIN RECEPTOR (O	2.38e-239
18	1240	55.6	228	1	OPRD_PIG DELTA-TYPE OPIOID RECE	7.95e-223
19	830	37.2	391	1	SSR1_RAT SOMATOSTATIN RECEPTOR	7.05e-138
20	830	37.2	391	1	SSR1_HUMAN SOMATOSTATIN RECEPTOR	7.05e-138
21	830	37.2	391	1	SSR1_MOUSE SOMATOSTATIN RECEPTOR	3.07e-136
22	822	36.9	384	1	SSR4_RAT SOMATOSTATIN RECEPTOR	5.20e-135
23	816	36.6	388	1	SSR4_HUMAN SOMATOSTATIN RECEPTOR	5.20e-135

24	810	36.3	384	1	SSR4_MOUSE SOMATOSTATIN RECEPTOR	8.78e-134
25	789	35.4	368	1	SSR2_BOVIN SOMATOSTATIN RECEPTOR	1.73e-129
26	789	35.4	369	1	SSR2_PIG SOMATOSTATIN RECEPTOR	1.73e-129
27	788	35.4	369	1	SSR2_RAT SOMATOSTATIN RECEPTOR	2.76e-129
28	785	35.2	369	1	SSR2_MOUSE SOMATOSTATIN RECEPTOR	1.13e-128
29	780	35.0	369	1	SSR2_HUMAN SOMATOSTATIN RECEPTOR	1.19e-127
30	736	33.0	333	1	GPR8_HUMAN PROBABLE G PROTEIN-COU	1.10e-118
31	696	31.2	362	1	SSR5_MOUSE SOMATOSTATIN RECEPTOR	1.45e-110
32	683	30.6	418	1	SSR3_HUMAN SOMATOSTATIN RECEPTOR	6.21e-108
33	676	30.3	363	1	SSR5_HUMAN SOMATOSTATIN RECEPTOR	1.62e-106
34	668	30.0	363	1	SSR5_RAT SOMATOSTATIN RECEPTOR	6.69e-105
35	661	29.7	328	1	GPR7_HUMAN PROBABLE G PROTEIN-COU	1.73e-103
36	635	28.5	98	1	OPRM_CAVPO MU-TYPE OPIOID RECEPTO	3.01e-98
37	601	27.0	428	1	SSR3_MOUSE SOMATOSTATIN RECEPTOR	2.02e-91
38	599	26.9	428	1	SSR3_MOUSE SOMATOSTATIN RECEPTOR	5.08e-91
39	545	24.5	349	1	GALR_HUMAN GALANIN RECEPTOR TYPE	3.00e-80
40	525	23.6	346	1	GALR_RAT GALANIN RECEPTOR TYPE	2.77e-76
41	521	23.4	348	1	GALR_MOUSE GALANIN RECEPTOR TYPE	1.71e-75
42	522	23.4	372	1	GALS_RAT GALANIN RECEPTOR TYPE	1.09e-75
43	510	22.9	402	1	GPRO_HUMAN PROBABLE G PROTEIN-COU	2.55e-73
44	496	22.3	355	1	CKR1_HUMAN C-C CHEMOKINE RECEPTOR	1.46e-70
45	496	22.3	359	1	AG2R_CANFA TYPE-1 ANGIOTENSIN II	1.46e-70

ALIGNMENTS

RESULT 1  
ID OPRK\_HUMAN STANDARD; PRT; 380 AA.  
AC P41145;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).  
GN OPRK1 OR OPRK.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-PLACENTA;  
RX MEDLINE; 94338360.  
RA MANSSON E., BARE L.A., YANG D.;  
RT "Isolation of a human kappa opioid receptor cDNA from placenta."  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-PLACENTA;  
RX MEDLINE; 95350200.  
RA SIMONIN F., GAVERIAUS-RUFF C., BEFORT K., LANNES B., MICHELETTI G.,  
RA MATTEI M.-G., CHARON G., BLOCH B., KIEFFER B.;  
RT "Kappa-Opioid receptor in humans: cDNA and genomic cloning,  
RT chromosomal assignment, functional expression, pharmacology, and  
RT expression pattern in the central nervous system."  
RL PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE; 95174504.  
RA ZHU J., CHEN C., XUE J.-C., KUNAPULI S., DERIEL J.K., LIU-CHEN L.-Y.;  
RT "Cloning of a human kappa opioid receptor from the brain."  
RL LIFE SCI. 56:201-207(1995).  
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC -----

DR EMBL; U11053; G532060; -.  
DR EMBL; U17298; G596070; -.  
DR EMBL; L37362; G722618; -.  
DR PIR; JC2338; JC2338.  
DR GCRDB; GCR\_1819; -.  
DR GCRDB; GCR\_2026; -.  
DR GCRDB; GCR\_2054; -.  
DR MIM; 165196; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.  
DR PFAM; PF00001; 7tm\_1; 1.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 174 196 4 (POTENTIAL).  
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOHYD 25 25 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
FT CONFLICT 2 2 E -> D (IN REF. 2 AND 3).  
SQ SEQUENCE 380 AA; 42659 MW; 1980629E CRC32;

EMBL; U04092; G476107; -.  
GCRDB; GCR\_0991; -.  
PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.  
PFAM; PF00001; 7tm\_1; 1.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 174 196 4 (POTENTIAL).  
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOHYD 25 25 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
SQ SEQUENCE 380 AA; 42736 MW; F9F34C4C CRC32;

Query Match 96.8%; Score 2157; DB 1; Length 380;  
Best Local Similarity 94.6%; Pred. No. 0.00e+00;  
Matches 279; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 87 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPGDVLCKIVISIDYNNMFTSI 146  
QY 1 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPGDVLCKIVISIDYNNMFTSI 60  
Db 147 FTLTMSVDRIYIACHPVKALDFRTPLKAKIINICIIWLLSSSVGISAIVLGGTKVREDVD 206  
QY 61 FTLTMSVDRIYIACHPVKALDFRTPLKAKIINICIIWLLSSSVGISAIVLGGTKVREDVD 120  
Db 207.IIECSLQFPDDDYSWWDLFMKICVFIFAFVPIVLIIVCYTLMILRLKSVRLLSGSREKD 266  
QY 121 VIECCLQFPDDDYSWWDLFMKICVFIFAFVPIVLIIVCYTLMILRLKXXVRLLSGSREKD 180  
Db 267 RNLRRITRLVVLVAVVVCWTPIHIFILVEALGSTSHSTAALSSYFICIALGYTNSSLN 326  
QY 181 XNLRITRLVVLVAVVVCWTPIHIFILVEALGSTSHSTAALSSYFICIALGYTNSSLN 240  
Db 327 PILYAFLDENFKRCFRDFCFPIKMRMERQSTSRVNTVQDPAYLRNVDGV-NKPV 380

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CC -----

DR EMBL; U11053; G532060; -.  
DR EMBL; U17298; G596070; -.  
DR EMBL; L37362; G722618; -.  
DR PIR; JC2338; JC2338.  
DR GCRDB; GCR\_1819; -.  
DR GCRDB; GCR\_2026; -.  
DR GCRDB; GCR\_2054; -.  
DR MIM; 165196; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.  
DR PFAM; PF00001; 7tm\_1; 1.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 174 196 4 (POTENTIAL).  
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOHYD 25 25 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
FT CONFLICT 2 2 E -> D (IN REF. 2 AND 3).  
SQ SEQUENCE 380 AA; 42659 MW; 1980629E CRC32;

Query Match 98.3%; Score 2192; DB 1; Length 380;  
Best Local Similarity 97.6%; Pred. No. 0.00e+00;  
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 87 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPGDVLCKIVISIDYNNMFTSI 146  
QY 1 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPGDVLCKIVISIDYNNMFTSI 60  
Db 147 FTLTMSVDRIYIACHPVKALDFRTPLKAKIINICIIWLLSSSVGISAIVLGGTKVREDVD 206  
QY 61 FTLTMSVDRIYIACHPVKALDFRTPLKAKIINICIIWLLSSSVGISAIVLGGTKVREDVD 120  
Db 207 VIECSLQFPDDDYSWWDLFMKICVFIFAFVPIVLIIVCYTLMILRLKSVRLLSGSREKD 266  
QY 121 VIECCLQFPDDDYSWWDLFMKICVFIFAFVPIVLIIVCYTLMILRLKXXVRLLSGSREKD 180  
Db 267 RNLRRITRLVVLVAVVVCWTPIHIFILVEALGSTSHSTAALSSYFICIALGYTNSSLN 326  
QY 181 XNLRITRLVVLVAVVVCWTPIHIFILVEALGSTSHSTAALSSYFICIALGYTNSSLN 240  
Db 327 PILYAFLDENFKRCFRDFCFPLKMRMERQSTSRVNTVQDPAYLRDIDGM-NKPV 380  
QY 241 PILYAFLDENFKRCFRDFCFPLKMXMERQSTSRVNTVQDPAYLRDIDGMNKPV 295

RESULT 2  
ID OPRK\_CAVPO STANDARD; PRT; 380 AA.  
AC P41144;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).  
GN OPRK1.  
OS CAVIA PORCELLUS (GUINEA PIG).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.

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QY 241 PILYAFLDENFKRCFRDFCFPLKMXMERXSTSRVNTVQDPAYLREIDGMMNKPV 295

RESULT 3
ID OPRK_MOUSE STANDARD; PRT; 380 AA.
AC P33534;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).
GN OPRK1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 93342064.
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
RA BELL G.I.;
RT "Cloning and functional comparison of kappa and delta opioid
RT receptors from mouse brain.";
RL PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95100967.
RA NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;
RT "Structure and chromosomal mapping of genes for the mouse
RT kappa-opioid receptor and an opioid receptor homologue (MOR-C).";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96084989.
RA BELKOWSKI S.M., ZHU J., LIU-CHEN L.Y., EISENSTEIN I.K.,
RA ADLER M.W., ROGERS T.J.;
RT "Sequence of kappa-opioid receptor cDNA in the R1.1 thymoma cell
RT line.";
RL J. NEUROIMMUNOL. 62:113-117(1995).
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: BRAIN (NEOCORTEX, HIPPOCAMPUS, AMYGDALA,
CC MEDIAL HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL
CC NUCLEUS).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC -----
CC EMBL; L11065; G348249; -
CC EMBL; D31665; G808876; -
CC EMBL; D31663; G808876; JOINED.
CC EMBL; D31664; G808876; JOINED.
CC EMBL; S77872; G998532; -
CC EMBL; S77868; G998532; JOINED.
CC EMBL; S77869; G998532; JOINED.
CC EMBL; S81111; E257489; -
CC PIR; A48227; A48227.
CC GCRDB; GCR_0635; -.
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DR GCRDB; GCR_1933; -
DR GCRDB; GCR_2355; -
DR MGD; MGI:97439; OPRK1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT IRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
FT CONFLICT 211 211 S -> L (IN REF. 2 AND 3).
FT CONFLICT 231 231 F -> V (IN REF. 2 AND 3).
SQ SEQUENCE 380 AA; 42652 MW; C6F33212 CRC32;

Query Match 95.8%; Score 2136; DB 1; Length 380;
Best Local Similarity 92.9%; Pred. No. 0.00e+00;
Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

Db 87 YTKMKTAINIYIFNLADALVTTTTPFQSAVYLMNSWPFQDVLCIKIVISIDYNNMFTSI 146
QY 1 YTKMKTATNIYIFNLADALVTTTTPFQSVYLMNSWPFQDVLCIKIVISIDYNNMFTSI 60

Db 147 FTLTMSVDYIAVCHPVKALDFRTPLKAKIINICIWLLASSVGISAIVLGGTKVREDVD 206
QY 61 FTLTMSVDYIAVCHPVKALDFRTPLKAKIINICIWLLSSVGISAIVLGGTKVREDVD 120

Db 207 VIECSLQFPDDYSWDLFMKICVFVFAFVPIVLIIVCYTLMILKSVRLLSGSREKD 266
QY 121 VIECSLQFPDDYSWDLFMKICVFVFAFVPIVLIIVCYTLMILKSVRLLSGSREKD 180

Db 267 RNLRRITKLVLVAVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYFICIALGYTNSSLN 326
QY 181 XNLRRITRLVLVAVVAVVAVVVCWTPIHIFILVEALGSTSHSTAALSSYFICIALGYTNSSLN 240

Db 327 PVLXAFLDENFKRCFRDFCFPIKMMERQSTNRVNTVQDPASMRDVGGM-NKPV 380
QY 241 PILYAFLDENFKRCFRDFCFPLKMXMERXSTSRVNTVQDPAYLREIDGMMNKPV 295

RESULT 4
ID OPRK_RAT STANDARD; PRT; 380 AA.
AC P34975;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN OPRK1 OR KOR-D.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94059008.
RA CHEN Y., MESTEK A., LIU J., YU L.;
RT "Molecular cloning of a rat kappa opioid receptor reveals sequence
RT similarities to the mu and delta opioid receptors.";
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Thu Feb 17 13:27:01 2000

US-08-455-683-12.rsp

RL BIOCHEM. J. 295:625-628(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93374033.
 RA MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,
 RA KANEKO S., SATOH M.;
 RT "Cloning and expression of a cDNA for the rat kappa-opioid receptor.";
 RL FEBS LETT. 329:291-295(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RX MEDLINE; 94059009.
 RA LI S., ZHU J., CHEN C., CHEN Y.-W., DERTEL J.K., ASHBY B.,
 RA LIU-CHEN L.-Y.;
 RT "Molecular cloning and expression of a rat kappa opioid receptor.";
 RL BIOCHEM. J. 295:629-633(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RX MEDLINE; 94052210.
 RA MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,
 RA WATSON S.J., AKIL H.;
 RT "Cloning and pharmacological characterization of a rat kappa opioid
 receptor.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=BRAIN;
 RX MEDLINE; 93380575.
 RA NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.;
 RT "cDNA cloning and pharmacological characterization of an opioid
 receptor with high affinities for kappa-subtype-selective ligands.";
 RL FEBS LETT. 330:77-80(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE; 95204422.
 RA YAKOVLEV A.G., KRUEGER K.E., FADEN A.I.;
 RT "Structure and expression of a rat kappa opioid receptor gene.";
 RL J. BIOL. CHEM. 270:6421-6424(1995).
 CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
 CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).
 CC -----
 DR EMBL; L22001; G409237; -
 DR EMBL; D16829; G404116; -
 DR EMBL; L22536; G425189; -
 DR EMBL; U00442; G403487; -
 DR EMBL; D16534; G415310; -
 DR EMBL; U17995; G727260; -
 DR EMBL; U17993; G727260; JOINED.
 DR EMBL; U17994; G727260; JOINED.
 DR PIR; S36143; S36143.
 DR PIR; S38825; S38825.
 DR GCRDB; GCR\_0636; -
 DR GCRDB; GCR\_0724; -
 DR GCRDB; GCR\_0790; -
 DR GCRDB; GCR\_0804; -
 DR GCRDB; GCR\_1282; -
 DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.
 DR PFAM; PF00001; 7tm\_1; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;

KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 59 85 1 (POTENTIAL).
 FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 96 117 2 (POTENTIAL).
 FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 133 154 3 (POTENTIAL).
 FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 174 196 4 (POTENTIAL).
 FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 223 247 5 (POTENTIAL).
 FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 276 299 6 (POTENTIAL).
 FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 312 333 7 (POTENTIAL).
 FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 131 210 BY SIMILARITY.
 FT LIPID 345 345 PALMITATE (POTENTIAL).
 FT CARBOHYD 25 25 POTENTIAL.
 FT CARBOHYD 39 39 POTENTIAL.
 FT CONFLICT 42 42 V -> L (IN REF. 2).
 FT CONFLICT 345 345 C -> Y (IN REF. 3).
 SQ SEQUENCE 380 AA; 42688 MW; EE858A46 CRC32;
 Query Match 95.6%; Score 2132; DB 1; Length 380;
 Best Local Similarity 92.5%; Pred. No. 0.00e+00;
 Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 YTKMKTATNIYIFNLALADALVTTTTPFQSAVYLMNSWFGDVLCKIVISIDYNNMFTSI 146
 QY 1 YTKMKTATNIYIFNLALADALVTTTTPFQSTVYLMNSWFGDVLCKIVISIDYNNMFTSI 60
 Db 147 FTLTMSVDRIYIAVCHPVKALDFTPLKAKIINICIWLLASSVGISAIVLGGTKVREDVD 206
 QY 61 FTLTMSVDRIYIAVCHPVKALDFTPLKAKIINICIWLLSSVGISAIVLGGTKVREDVD 120
 Db 207 VIECSLQFPDDDEYSWDLFMKICVVFVAFVPIVLIIVCYILMLRLKSVRLLSGSREKD 266
 QY 121 VIECCQLQFPDDDYSDWDLFMKICVVFVAFVPIVLIIVCYILMLRLKSVRLLSGSREKD 180
 Db 267 RNLRRITKLVLVVAVFIICWTPIHIFILVEALGSTSHSTAVLSSYFICIALGYTNSSLN 326
 QY 181 XNLRRITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAAALSSYFICIALGYTNSSLN 240
 Db 327 PVLVAFLDENFKRCRDFCFPIKMRMERQSTNRVNTVQDPASMRDVGGM-NKPV 380
 QY 241 PVLVAFLDENFKRCRDFCFPLKMXMERXSTSRVNTVQDPAYLRIDGMNKPV 295
 RESULT 5
 ID OPRM\_MOUSE STANDARD; PRT; 398 AA.
 AC P42866; Q60768;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE M7-TYPE OPIOID RECEPTOR (MOR-1).
 GN OPRM1 OR OPRM OR MOR.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=LIVER;
 RX MEDLINE; 94377496.
 RA MIN B.H.; AUGUSTIN L.B., FELSHEIM R.F., FUCHS J.A., LOH H.H.;
 RT "Genomic structure analysis of promoter sequence of a mouse mu opioid
 receptor gene.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 91:9081-9085(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE; 95377399.
 RA ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.;



RN SEQUENCE OF 101-340 FROM N.A.
RP TISSUE=MACROPHAGE;
RX MEDLINE; 95251654.
RA SEDQI M., ROY S., RAMAKRISHNAN S., ELDE R., LOH H.H.;
RT "Complementary DNA cloning of a mu-opioid receptor from rat
peritoneal macrophages.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 209:563-574(1995).
RN SEQUENCE OF 356-391 FROM N.A.
RP MEDLINE; 95172221.
RX ZIMPRICH A., SIMON T., HOLLT V.;
RA "Cloning and expression of an isoform of the rat mu opioid receptor
(rMOR1B) which differs in agonist induced desensitization from
rMOR1.";
RL FEBS LETT. 359:142-146(1995).
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR BETA-ENDORPHIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: BRAIN. IS EXPRESSED IN THE CEREBRAL CORTEX,
CAUDATE PUTAMEN, NUCLEUS ACCUMBENS, SEPTAL NUCLEI, THALAMUS,
HIPPOCAMPUS, AND HABENULA. NOT DETECTED IN CEREBELLUM.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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EMBL; D16349; G391867; -
DR EMBL; L20684; G409150; -
DR EMBL; L13069; G348251; -
DR EMBL; U02083; G403574; -
DR EMBL; L22455; G437672; -
DR EMBL; U35424; G1017732; -
DR EMBL; S77863; E199500; -
DR EMBL; S75669; G861432; -
DR PIR; S34593; S34593.
DR GCRDB; GCR\_0633; -
DR GCRDB; GCR\_0637; -
DR GCRDB; GCR\_0639; -
DR GCRDB; GCR\_0640; -
DR GCRDB; GCR\_0864; -
DR GCRDB; GCR\_1101; -
DR GCRDB; GCR\_1425; -
DR GCRDB; GCR\_2361; -
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.
DR PFAM; PF00001; 7tm\_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 64
FT TRANSMEM 65 94
FT DOMAIN 95 103
FT TRANSMEM 104 121
FT DOMAIN 122 143
FT TRANSMEM 144 163
FT DOMAIN 164 193
FT TRANSMEM 194 209
FT DOMAIN 210 234
FT TRANSMEM 235 257
FT DOMAIN 258 280
FT TRANSMEM 281 303
FT DOMAIN 304 311
FT TRANSMEM 312 328
FT TRANSMEM 329 398
FT DOMAIN 140 217
FT DISULFID 351
FT LIPID 351
FT CARBOHYD 9
FT CARBOHYD 31
POTENTIAL.

FT CARBOHYD 38 38 POTENTIAL.
FT CARBOHYD 46 46 POTENTIAL.
FT CARBOHYD 53 53 POTENTIAL.
FT CONFLICT 237 237 F -> G (IN REF. 6).
FT CONFLICT 245 245 V -> I (IN REF. 3, 4 AND 7).
FT CONFLICT 391 391 LENLE -> KIVLF (IN REF. 8).
SQ SEQUENCE 398 AA; 44494 MW; 2C21013D CRC32;

Query Match 68.3%; Score 1522; DB 1; Length 398;
Best Local Similarity 66.1%; Pred. No. 5.72e-282;
Matches 191; Conservative 45; Mismatches 49; Indels 4; Gaps 4;

Db 96 YTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSI 155
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 YTKMKTATNIYIFNLALADALVTTTTPFQSTVYLMNSWFFGDLVLCCKIVISIDYNNMFTSI 60

Db 156 FTLCMTSVDRYIAVCHPVKALDFRTPRNAKIVNVCNWLSSAIGLPMFMATTKYRQG-S 214
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 FTLTMSVDRYIAVCHPVKALDFRTPLKAKIINICINLSSVSGISAIVLGGTKVREDVD 120

Db 215 -IDCTLTFSHPTW-YWENLLKICVFIFAFIMPVLIITVCYGLMILRLKSVRLSGSKEKD 272
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 VIECCLQFPDDDDYSWDLFMKICVFIFAFVPLIIIVCYTLMILRLKXXVRLSGSREKD 180

Db 273 RNLRRITRMVLVVAVFIVCVTPHIIYVVIKALITIPETTFQTVSWHFCIALGYTNSCLN 332
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 XNLRRITRLVLVVAVFVVCVTPHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN 240

Db 333 PVLVAFLDENFKRCFREFCIPTESSIEQQNSTVRQNTREHPSTANTVD 381
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 PILVAFLDENFKRCFRDFCFPLKMXMERXSTSRVR-NTVQDPAYLREID 288

RESULT 7
ID OPRM\_HUMAN STANDARD; PRT; 400 AA.
AC P35372; Q12930;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1 OR MOR1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94139928.
RA WANG J.-B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,
RA UHL G.R.;
RT "Human mu opiate receptor. cDNA and genomic clones, pharmacologic
RT characterization and chromosomal assignment.";
RL FEBS LETT. 338:217-222(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA MESTEK A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M.,
RA CHEN Y., YU L.;
RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 95046336.
RA BARE L.A., MANSSON E., YANG D.;
RT "Expression of two variants of the human mu opioid receptor mRNA in
RT SK-N-SH cells and human brain.";
RL FEBS LETT. 354:213-216(1994).
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR BETA-ENDORPHIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----



[illegible]

RESULT	9	STANDARD;	PRT;	401 AA.
ID	OPRM BOVIN			
AC	P79350;			
DT	15-JUL-1998	(REL. 36, CREATED)		
DT	15-JUL-1998	(REL. 36, LAST SEQUENCE UPDATE)		
DT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)		
DE	MU-TYPE OPIOID RECEPTOR (MOR-1).			

OC ARTIODACTYLTA; RUMINANTIA; PECORA; BOVULDEA; BOVINAE; BOS;  
[1]  
RN SEQUENCE FROM N.A.

RA SIMON E.J., VILLEM S., ANDRIA M.; UNOFRISHVIDI I.;  
PI SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

CC ION CURRENTS AND INCREASING POTASSIUM CONDUCTANCE. RECEPTION  
CC FOR PETA-ENDORPHIN

CC    != SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN

CC    != SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COU

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[illegible]

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DR EMBL; 005077; G1001051;
DR GCRDB; GCR_1213; -.
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DR PFAM; PF00001; 7tm\_1; 1.

KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.

FT	TRANSMEM	68	97	1 (POTENTIAL).

FT	TRANSMEM	107	124	2 (POTENTIAL).	EVERY CELL IN AP. (POTENTIAL)
FT	TRANSMEM	107	124	2 (POTENTIAL).	EVERY CELL IN AP. (POTENTIAL)

FT	TRANSMEM	147	166	3 (POTENTIAL).
FT	DOUAIN	167	105	CYTOPLASMIC (POTENTIAL)

FT	TRANSMEM	197	212	4 (POTENTIAL).
FT <td>DOMAIN <td>213 <td>237 <td>EXTRACELLULAR (POTENTIAL).</td> </td></td></td>	DOMAIN <td>213 <td>237 <td>EXTRACELLULAR (POTENTIAL).</td> </td></td>	213 <td>237 <td>EXTRACELLULAR (POTENTIAL).</td> </td>	237 <td>EXTRACELLULAR (POTENTIAL).</td>	EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	238	260	3 (POTENTIAL):
FT	DOMAIN	261	283	CYTOPLASMIC (POTENTIAL):

FT	TRANSMEM	284	300	309 (POTENTIAL).	EXTRACELLULAR (POTENTIAL).
FT <td>DOMAIN <td>307 <td>314 <td></td> <td></td> </td></td></td>	DOMAIN <td>307 <td>314 <td></td> <td></td> </td></td>	307 <td>314 <td></td> <td></td> </td>	314 <td></td> <td></td>		

FT	DOMAIN	332	401	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	332	401	CYTOPLASMIC (POTENTIAL).

FT	CARBOHYD	9	POTENTIAL.
FT		9	

FT	CARBOHYD	34	34	POTENTIAL.
FT	CARBOHYD	34	34	POTENTIAL.

FT	CARBOHYD	49	49	POTENTIAL.	
					56738089 CBC23.

cc 98. 1189. DB 1. Length

Best Local Similarity 66.1%; Pred. No. 5.00e-273;

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN CORTEX, AND STRIATUM;

KNAPP R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M.

"Identification of a human delta opioid receptor: cloning and

RL LIFE SCI. 54:463-469(1994).

RP SEQUENCE FROM N. A.

RA SIMONIN F., BEFORT K., GAVERIAUX-RUFF C., MATTHES H., NAPPEY

"The human delta-opioid receptor: genomic organization, cDNA functional expression and distribution in human brain."

RL MOL. PHARMACOL. 46:1015-1021(1994).

RP SEQUENCE FROM N.A.  
BA GRAHAM D :

CC  
RT  
SUBMITTED (FEB-1998) TO EMBO/ GENARK/ DDO JOURN. BOARD.  
-!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING C

ION CURRENTS AND ENKEPHALIN RECEPTOR FOR ENKEPHALINS. STEREOSSELECTIVE.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS

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DR EMBL; U07882; G497314; -  
DR FMRL; U10504; G501145; -

DR EMBL; AL009181; E1230308; -;  
DR GCRDB: GCR 1017: -;

DR GCRDB; GCR\_2055; -.  
DR MIM; 165195; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.  
DR PFAM; PF00001; 7tm\_1; 1.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 45  
FT TRANSMEM 46 75  
FT DOMAIN 76 84  
FT TRANSMEM 85 102  
FT DOMAIN 103 124  
FT TRANSMEM 125 144  
FT DOMAIN 145 174  
FT TRANSMEM 175 190  
FT DOMAIN 191 215  
FT TRANSMEM 216 238  
FT DOMAIN 239 261  
FT TRANSMEM 262 284  
FT DOMAIN 285 293  
FT TRANSMEM 294 310  
FT DOMAIN 311 372  
FT CARBOHYD 18 18  
FT CARBOHYD 33 33  
FT DISULFID 121 198  
FT LIPID 333 333  
FT CONFLICT 27 27  
FT CONFLICT 40 41  
FT CONFLICT 348 348  
FT CONFLICT 370 370  
SQ SEQUENCE 372 AA; 40368 MW; 4A57DD07 CRC32;

Query Match 65.4%; Score 1458; DB 1; Length 372;  
Best Local Similarity 69.2%; Pred. No. 1.64e-268;  
Matches 180; Conservative 43; Mismatches 33; Indels 4; Gaps 4;

Db 77 YTKMKTATNIYIFNLALADALATSTLPFQSAKYLMETWPFGLLCKAVLSIDYNNMFTSI 136  
QY 1 YTKMKTATNIYIFNLALADALVTTTTPFQSTVYLMNSWPFGLVCKIVISIDYNNMFTSI 60  
Db 137 FTLTMSVDRIYAVCHPVKALDERTPAKAKLINICIWVLASGVGPIMVAVTRPDGA- 195  
QY 61 FTLTMSVDRIYAVCHPVKALDERTPLKAKLINICIWLLSSVGSIAVLGGIKVREDVD 120  
Db 196 VV-CMLQFPSPW-YWDTVTKICVFLFAFVVPVILITVVCYGLMLRLRSVRLLSGSKEKD 253  
QY 121 VIECCLQFPDDYSWWDLFMKICVFIFAFVFPVLIIVCYTLMILRLKXVRLLSGSREKD 180  
Db 254 RSLRRITRMVLVVVGAFVVCWAPIHIFVIVWILVDIDRRDPLVVAALHLCIALGYANSSL 313  
QY 181 XNLRITRLVVLVAVFVVCWTPHIFILVEALGSTSHSTA-ALSSYFICIALGYTNSSL 239  
Db 314 NPVLYAFLDENKRCRQLC 333  
QY 240 NPILYAFLDENKRCRDFC 259

RESULT 11  
ID OPD\_RAT STANDARD; PRT; 372 AA.  
AC P33533;  
DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).  
GN OPD1 OR ROR-A.  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE; 93351652.  
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;  
RT "Primary structures and expression from cDNAs of rat opioid receptor

RT delta- and mu-subtypes.";  
RL FEBS LETT. 327:311-314(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RX MEDLINE; 94322412.  
RA ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;  
RT "Molecular cloning and expression of a delta-opioid receptor from rat brain";  
RL J. NEUROSCI. RES. 37:714-719(1994).  
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
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CC -----

EMBL; D16348; G391865; -.  
DR EMBL; U00475; G514211; -.  
DR PIR; S34592; S34592.  
DR GCRDB; GCR\_0638; -.  
DR GCRDB; GCR\_0805; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.  
DR PFAM; PF00001; 7tm\_1; 1.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 45  
FT TRANSMEM 46 75  
FT DOMAIN 76 84  
FT TRANSMEM 85 102  
FT DOMAIN 103 124  
FT TRANSMEM 125 144  
FT DOMAIN 145 174  
FT TRANSMEM 175 190  
FT DOMAIN 191 215  
FT TRANSMEM 216 238  
FT DOMAIN 239 261  
FT TRANSMEM 262 284  
FT DOMAIN 285 293  
FT TRANSMEM 294 310  
FT DOMAIN 311 372  
FT CARBOHYD 18 18  
FT CARBOHYD 33 33  
FT DISULFID 121 198  
FT LIPID 333 333  
SQ SEQUENCE 372 AA; 40449 MW; 59F5EE50 CRC32;

Query Match 65.1%; Score 1452; DB 1; Length 372;  
Best Local Similarity 68.8%; Pred. No. 2.99e-267;  
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

Db 77 YTKLKTATNIYIFNLALADALATSTLPFQSAKYLMETWPFGLLCKAVLSIDYNNMFTSI 136  
QY 1 YTKMKTATNIYIFNLALADALVTTTTPFQSTVYLMNSWPFGLVCKIVISIDYNNMFTSI 60  
Db 137 FTLTMSVDRIYAVCHPVKALDERTPAKAKLINICIWVLASGVGPIMVAVTRPDGA- 195  
QY 61 FTLTMSVDRIYAVCHPVKALDERTPLKAKLINICIWLLSSVGSIAVLGGIKVREDVD 120  
Db 196 VV-CILQFPSPW-YWDTVTKICVFLFAFVVPVILITVVCYGLMLRLRSVRLLSGSKEKD 253  
QY 121 VIECCLQFPDDYSWWDLFMKICVFIFAFVFPVLIIVCYTLMILRLKXVRLLSGSREKD 180  
Db 254 RSLRRITRMVLVVVGAFVVCWAPIHIFVIVWILVDINRRDPLVVAALHLCIALGYANSSL 313  
QY 181 XNLRITRLVVLVAVFVVCWIPHIFILVEALGSTSHSTA-ALSSYFICIALGYTNSSL 239





QY 241 PILYAFLDENFKRCRDFCFPLKMXMERXSTSRVNTVQD 280  
|||||

RESULT 14  
ID OPRX\_MOUSE STANDARD; PRT; 367 AA.  
AC P35377; Q60645;  
DT 01-JUN-1994 (REL. 29, CREATED)  
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID  
RECEPTOR) (KOR-3) (ORGC) (K3 OPIATE RECEPTOR).  
GN OPR11 OR OPR1 OR OOR.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6N; TISSUE=BRAIN;  
RA VASUDA K., JONES E., REISINE T., BELL G.I.;  
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95100967.  
RA NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;  
RT "Structure and chromosomal mapping of genes for the mouse  
kappa-opioid receptor and an opioid receptor homologue (MOR-C).";  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 96387345.  
RA MATHES H.W.D., SEWARD E.P., KIEFFER B., NORTH R.A.;  
RT "Functional selectivity of orphanin FQ for its receptor coexpressed  
with potassium channel subunits in Xenopus laevis oocytes.";  
RL MOL. PHARMACOL. 50:447-450(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA PAN Y.-X., XU J., PASTERNAK G.W.;  
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95327076.  
RA PAN Y.-X., CHENG J., XU J., ROSSI G., JACOBSON E., RYAN-MORO J.,  
RA BROOKS A.I., DEAN G.E., STANDIFER K.M., PASTERNAK G.W.;  
RT "Cloning and functional characterization through antisense mapping of  
a kappa 3-related opioid receptor";  
RL MOL. PHARMACOL. 47:1180-1188(1995).  
RN [6]  
RP SEQUENCE OF 1-357 FROM N.A.  
RC STRAIN=BALE/C; TISSUE=SPLEEN;  
RX MEDLINE; 95318231.  
RA HALFORD W.P., GEBHARDT B.M., CARR D.J.J.;  
RT "Functional role and sequence analysis of a lymphocyte orphan opioid  
receptor";  
RL J. NEUROIMMUNOL. 59:91-101(1995).  
CC -!- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.  
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,  
CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF  
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYL  
CC CYCLASE.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----

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-----  
EMBL; U04952; G440880; -.

DR EMBL; D31667; G80874; -.  
DR EMBL; D31666; G80874; JOINED.  
DR EMBL; X91813; G1008982; -.  
DR EMBL; U32932; G1464791; -.  
DR EMBL; U32928; G1464791; JOINED.  
DR EMBL; U32930; G1464791; JOINED.  
DR EMBL; U09421; G551485; -.  
DR EMBL; U14165; G540093; -.  
DR GCRDB; GCR\_0891; -.  
DR GCRDB; GCR\_1715; -.  
DR GCRDB; GCR\_1716; -.  
DR GCRDB; GCR\_1728; -.  
DR GCRDB; GCR\_1731; -.  
DR MGD; MGI:97440; OPR1.  
DR PROSITE; PS00237; G.PROTEIN\_RECEPTOR; 1.  
DR PFAM; PF00001; 7tm\_1; 1.  
DR HSSP; P34996; 1DDD.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 48 74 1 (POTENTIAL).  
FT DOMAIN 75 84 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 85 106 2 (POTENTIAL).  
FT DOMAIN 107 121 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 122 143 3 (POTENTIAL).  
FT DOMAIN 144 162 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 163 185 4 (POTENTIAL).  
FT DOMAIN 186 208 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 209 233 5 (POTENTIAL).  
FT DOMAIN 234 261 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 262 285 6 (POTENTIAL).  
FT DOMAIN 286 297 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 298 319 7 (POTENTIAL).  
FT DOMAIN 320 366 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 120 197 BY SIMILARITY.  
FT LIPID 331 331 PALMITATE (POTENTIAL).  
FT CARBOHYD 21 21 POTENTIAL.  
FT CARBOHYD 26 26 POTENTIAL.  
FT CARBOHYD 36 36 POTENTIAL.  
FT CONFLICT 348 349 SI -> TV (IN REF. 2).  
SQ SEQUENCE 367 AA; 40491 MW; 3F472156 CRC32;

Query Match 60.3%; Score 1343; DB 1; Length 367;  
Best Local Similarity 62.1%; Pred. No. 2.23e-244;  
Matches 174; Conservative 46; Mismatches 55; Indels 5; Gaps 5;

Db 77 TKMKTATNIYIFNLADTLVLLTLPFQGTDLILGFWFPGNALCKTVIAIDYNNFTSTF 136  
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QY 2 TKMKTATNIYIFNLADALVTTTTPFQSTVYLMNSWPFQDVLCCKIVISIDYNNFTSIF 61  
Db 137 TLTAMSVDRYVAICHPIRALDVRTSSKAQAVNVAIWALASVGVGPVAIMGSAQV-EDEE- 194  
|||||  
QY 62 ILTMSVDRYIAVCHPVPKALDFRTPLKAKIINICINLSSSVGISAIVLGGTKVREDVDV 121  
Db 195 IECLVEIPAPQDY-WGPVEA-ICIFLFSFIIPVLIISVCYSIMIRLRGVRLLSGREKD 252  
|||||  
QY 122 IECLQFPD-DDYSWDLFMKICVFIFAFVPIVLIITVCTLMILRLKXXVRLLSGREKD 180  
Db 253 RNLRITRLVLVVAVFVGWTPVQVFLVQGLGVQPGVQSETAVAILRFTALGYVNSCLN 312  
|||||  
QY 181 XNLRITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYINSSLN 240  
Db 313 PILYAFLDENFKACFRKCCASALHREMOMQVSDRVRISIAKD 352  
|||||  
QY 241 PILYAFLDENFKRCRDFCFPLKMXMERXSTSRVNTVQD 280

RESULT 15  
ID OPRX\_HUMAN STANDARD; PRT; 370 AA.  
AC P41146;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID  
DE RECEPTOR) (KOR-3).  
GN OPR1 OR ORL1 OR OOR.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-BRAIN STEM;  
RC MEDLINE; 94185768.  
RA MOLLEREAU C., PARMENTIER M., MAILLEUX P., BUTOUR J.L., MOISAND C.,  
RA CHALON P., CAPUT D., VASSART G., MEUNIER C.;  
RT "ORL1, a novel member of the opioid receptor family. Cloning,  
RT functional expression and localization.";  
RL FEBS LETT. 341:33-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA LEE P.H., ZHU J., LIU-CHEN L., CHANG K.;  
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -!- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.  
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,  
CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF  
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL  
CC CYCLASE.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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CC -----  
DR EMBL; X77130; G471317; -.  
DR EMBL; U30185; G1144297; -.  
DR PIR; S43087; S43087.  
DR GCRDB; GCR\_0987; -.  
DR GCRDB; GCR\_1988; -.  
DR MIM; 602548; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; 1.  
DR PFAM; PF00001; 7tm\_1; 1.  
DR HSSP; P34996; 1DDD.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
FT PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 50 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 51 77 1 (POTENTIAL).  
FT DOMAIN 78 87 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 88 109 2 (POTENTIAL).  
FT DOMAIN 110 124 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 125 146 3 (POTENTIAL).  
FT DOMAIN 147 165 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 166 188 4 (POTENTIAL).  
FT DOMAIN 189 211 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 212 236 5 (POTENTIAL).  
FT DOMAIN 237 264 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 265 288 6 (POTENTIAL).  
FT DOMAIN 289 300 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 301 322 7 (POTENTIAL).  
FT DOMAIN 323 370 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 123 200 BY SIMILARITY.  
FT LIPID 334 334 PALMITATE (POTENTIAL).  
FT CARBOHYD 21 21 POTENTIAL.  
FT CARBOHYD 28 28 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
SQ SEQUENCE 370 AA; 40693 MW; BE3C3E8F CRC32;

Query Match 59.7%; Score 1331; DB 1; Length 370;  
Best Local Similarity 60.6%; Pred. No. 7.28e-242;  
Matches 171; Conservative 49; Mismatches 57; Indels 5; Gaps 5;

Db 80 TKMTATNIYIFNLALADILVLLTLPFOGTDILLGFWPFGNALCKTVIAIDYNNMTSTF 139

QY 2 TKMTATNIYIFNLALADILVLLTLPFOGTDIVLMSWDFGDLCKIVISIDYNNMTSIF 61  
Db 140 TLTAMSVDRYVAICHPIRALDVRTSSKAQAVNVAIWALASVGVPAIMGSAQV-EDEE- 197  
QY 62 TLTAMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDV 121  
Db 198 IECLVEIPTQDY-WGPVFA-ICIFLFSFIVPVLVISVCYSLMIRLRGVRLLSGSREKD 255  
QY 122 IECCLOFPD-DDYSWWDLFMKICVFIFAFVIVPVLIIIVCYTLMILRLKXXVRLLSGSREKD 180  
Db 256 RNLRRITRLVVLVVAVFVGCWTPVQVFLAQGLGVQPSSETAVAILRFECTALGYVNSCLN 315  
QY 181 XNLRRITRLVVLVVAVFVGCWTPVHIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN 240  
Db 315 PILYAFLDENFKACERKFCASALRRDQVSDRVSIAKDVA 357  
QY 241 PILYAFLDENFKRCFRDFCFPLKMMXMERXSTSRVENTVQDPA 282

Search completed: Thu Feb 17 11:16:19 2000  
Job time : 12 secs.

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